### **SEARCH REQUEST FORM**

Requestor's Name:		erial umber:	
Date:	Phone:	Art Unit:	
Search Topic: Please write a detailed statement of set that may have a special meaning. Give a copy of the sequence. You may income the sequence of the sequence.	e examples or relevant citations, author	ossible the subject matter to be searche ors keywords, etc., if known. For sequ nost relevant claim(s).	d. Define any terms tences, please attach
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Mammalia; Eutheria;
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Sequence 1 from patent US 6280955.
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	AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal	361	Q
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HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATC	490	дb
rMetGly 1	ProAsnValAspGlyTyrPheProSerSerValLysProThrIl	161	Ş
CAGAGGATCACTTGT 489	CCCATGAAACTCCCAGTGCATAAACTGTATATAGAATATGGCATT	430	Db
ThrCys 1	ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIl	141	ঠ
CTGTTTCAATTCC 429	TATTGCAGCAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAC	370	Db
CysPheAs	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSe	121	S S
AAGGAACACTACA 369	TICCGGCCCACTCCCTCAATGACACTGGCAACTATACCTGCATGTT	310	Db 49
GATGIGCIGIGG 30	GAGCCAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGA	250	ם י
SASPValLeuTrp 100	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLy	. 81	. S
CCGGGACCT	GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGG	190	Дb
spArgAspLeuGlu 80	AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAs	61	δ
CAACTACAGCACA 189	GAGCCAGCTCGCATCAAGTGCCCCACTCTTGAACACTTCTTGAAATI	130	Дb
eAsnTyrSerThr 6	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPh	41	δ
	TCAGAACGCTGCGATGACTGGGGACTAGACA	70	라
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GCAAAGTGATGCC 69	ATGROACTTCTGTGTGTGTGTGTGAGTCTGTACTTTTATGGAATCCTG	10	ㅠ

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                                                                              Huang, J., Gao, X., Li, S. and Cao, Z.
Direct Submission
Submitted (07-OCT-1997) Biology, To
South San Francisco, CA 94080, USA
Location/Qualifiers
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Gatarrhini; Hominidae; Homo.

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Huang, J., Gao, X., Li, S. and Cao, Z.

Recruitment of IRAK to the interleukin 1 receptor complex requires interleukin 1 receptor accessory protein

Proc. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)
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Percent Similarity:
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95293970
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Direct Submission
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Mammalia; Eutheria;
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1. Biol. Chem. 270 (23), 13757-13765 (1995)
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/db xref="taxon:10090"
/cell line="3T3-L1"
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400 1334	381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400 	음 성
380 1274	361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal	용 성
360 1214	341 ValalalysalaalalysVallysGlnLysValProalaProArgTyrThrValGluLeu :::	당 성
340 1154	321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	.B &
320 1094	301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys.    :::   ::	B 8
300 1034	281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu:	용 성
280 974	261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal :	닭
260 914	241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu::::	. 문 왕
240 854	221 ArgThrPheHisLeuThrArgThrLeuThrValLy8ValValGlySerProLysAsnAla :	용 성
220 794	201 IleAlaLeuIleSerAsnAsnGlýAsnTyrThrCysValValThrTyrProGluAsnGly :	용 성
200 734	181 CysTyrLysIleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeuSefPheLeu :	유 성
180 674	161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 1	음 성
160 614	141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 1	유왕
140	121 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 1	Д <b>ь</b>
120 494	101 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 1	음 성
100	81 GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 1 {	용 성
80 374	61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu E	유왕
60 314	41 GluproAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 6	문 왕
254	195 TCGGAGCGCTGTGATGACTGGGGACTAGATACCATGCGACAAATCCAAGTGTTTGAAGAT 2	皮

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GTCATTTTAGTGCAGTACAAAGCTGTGAAGGACATGAAG-----GTGAAAGAGCTGAAG
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Liu,C., Chalmers,D., Maki,R. and De Souza,E.B.
Rat homolog of mouse interleukin-1 receptor accessory protein:
cloning, localization and modulation studies
J. Neuroimmunol. 66 (1-2), 41-48 (1996)
                                                                                                                                                                                                                                                                                                      U48592
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                    Submitted (06-FEB-1996) Changlu Biosciences, Inc., 3050 Science Location/Qualifiers
                                                                                                                                                                                                                            Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Rattus norvegicus interleukin-1
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organism="Rattus norvegicus"/
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                                           Liu,
Park
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                                         Molecular Biology, Neurocrine
RD, San Diego, CA 92121, USA
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TGTACTGAAATAGTGAATTTTCATAATGTTCAACCCAAGGGCATGAACTTGAGTTTTTTC
             CysTyrLysIleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeuSerPheLeu 200
                                                                            ProAsnValAspGlýTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
                                                                                                                                                                                       TACTGCAGCAAAGTTGCATTTCCCCTGGAAGTTGTTCAGAAGGACAGCTGTTTCAATTCC
                                                                                                                                                                                                            TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
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                                                                                                                                                                                                                                                                        PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
                                                             CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCATCGGTCACTTGGTATAAGGGT
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NGRLFHLIRTMYVKVVGSPKDAVPPHI'SSNDRVVYEKEFGEELVJPCKVYFSPMDS
HNEIMWTIDGKKPDDVPUDITIESVSYSSTEDETRTQILSIKKVTPEDLKRNYVCHA
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	AlaSerSerGlvTrnAsnGluSer 558	551	Ş	
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rLeuSer 550	uArgLeuAlaLeuProLeuArgSe	531	Ş	
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'n	::::::          :: GTGAAGGACTTGAJ	1594	뮍	
51	/alGluTyrArgProLeuGluHisProHisProGlyIleLeuG	497	.: Q	
TCAAC 15	:::::   ::::::::::::::::::::::::::::::	1543	뮹 .	
!	.ysLeuGlyValMetCysGlnAsnSerIleAlaThrLys	481	S	
AGCCCTC 1542		1483	Db	
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TCAGAAA 1482		1423	Дb	
_Ω	pArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheI	441	Ś	
CATCITC 1422	GTGCTGCTGACACTACGTGGAGTTTTTGGAGAATGAGTTCGGATACAAGCTGTG	1363	дь	
- 51	.ThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCy	421	ð	
AGAGTTT 1362	GACGGAAAAGAATATGATATTTATGTTTCCTATGCAAGAAATGCAGAAGAAGAAGAA	1303	Db	•
uGluPhe 420	pGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAla	401	Ş	
AATTCTT 1302	TCATTTTG	1243	Db	
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CCACGTT 1242	reereer	1183	_ Db	
- Œ	sGlyPheGlyAlaThrValLeuLeuValValI	361	ş	
AGAACTC 1182	GCCGAGCAAGCAGCCAAGGTGAAACAGAAAGTCATACCGCCAAGGTACACAGTAG	1123	. <b>Dp</b>	
uLe	ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrVa	341	ঠ	
HIIIII AGGGGAA 1122	GTCACCCCTGAGGATCTGAAGCGCAACTATGTCTGTCACGCTCGAAATGCCGAAGGGGAA	1063	Дb	
sGlyGlu 340	nrSerGluAspLeuLysArgSerTyrValCysHi	321	Ş	
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oglyglu 260	ValProProVallleHisSerProAsnAsp	241	β	
GGATGCA 822	CGGCTCTTTCAC	763	ф	
snAl	rPheHisLeuThrArgThrLeuThrValLysValValGlySerI	221	φ	
ACGGA 7	ATCCCCTTGGTATCAAATAACGGAAATTACACATGTGTGGTGACGTATCTGGAAA	703	В	
uAsnGly 220	leAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrF	201	Ş,	

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551 AlaSerSerGlyTrpAsnGluSer 558

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                                ---AGTCCCAGGTGGTCTAGCAGT 1773
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Homo sapiens soluble interleukin-l receptor accessory protein
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Jensen, L.E.
Direct Submission
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1 (bases 1 to 1857)

Jensen, L.E., Muzio, M., Mantovani, A. and Whitehead, A.S.

IL-1 signaling cascade in liver cells and the involvement of a soluble form of the IL-1 receptor accessory protein

Soluble form of the IL-1 receptor accessory protein

J. Immunol 164 (10), 5277-5286 (2000)
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RSAKGEVAKAAKVKQKGNRCGQ"
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	41 ValalatysAlaAlatysValtysGlntys 350 	Оу 34 рь 102	
1020	1 GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCGAA	Db 96	
340	1 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	Qy 32	
960	01 AGTATAAGTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAA	9	
320	1 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys	0у 30	
900	1 TGGTGGACCATTGATGGAAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA	œ.	
300	1 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu	Qy 28	
840	1 GAGCTACTCCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT		
280	1 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnG	0у 26	
780	1 GTGCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAA	7	
260	1 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu	Qy 24	
720	1 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA	Db 66	
240	1 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla	Qy 22	
099	1 ATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGA	Db 60	
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180	1 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly	0у 16	
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160	1 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys	Qy 14	
420	1 TATTGCAGCAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC	Db 36	
140	1 TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer	Qy 12	
360	1 TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACA	Db 30	
120	1 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	Qy 10	
300	1 GAGCCAATTAACTTCCGCCTCCCCGGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG	Db 24	
100	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	Qy 8	
240	1 GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGACCTTGAG	Db 18	
80	1 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu	Qy 6	
180	1 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAAATTCAACTACAGCACA	<u>-</u> ب	
60	1 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	Qy 4	
120		Db 6	

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TITLE
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MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla
                                                                       ATGGGACTTCTGTGGTATTTGATGAGTCTGTCCTTATGGGATCCTGCAGAGTCATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Pahey, Erin Helton, Mark Kettem
Madan, Stephanie Rodrigues, Amy Sanchez and Michell
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MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 18 Row: i Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6680420 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R.
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Mammalia; Eutheria;
1 (bases 1 to 1916)
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/db_xref="GI:18088148"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Liver, normal. 5
/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="Similar to interleukin
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/db_xref="taxon:10090"
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VERSION KEYWORDS

ACCESSION

to Homo sapiens AK095107 AK095107.1 GI: oligo capping;

Homo AK095107

5107 2226 bp mRNA linear sapiens cDNA FLJ37788 fis, clone BRHIP2028593, omo sapiens IL-1 receptor accessory protein mRN

PRI 15-JUL-2002 weakly similar

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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kodaira, H., Furuya, T., Takahashi, M., Kikkawa, B., Omura, Y., Abe, K. Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T. Nagohand, DNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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Isogai, T. and Yamamoto, J.
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PHPGILQLKESVSFVSWKGEKSKHSGSKFWKALRLALPLRSLSASSGWNESCSSQSDI
SLDHVQRRRSRLKEPPELQSSERAAGSPPAPGTMSKHRGKSSATCRCCVTYCEGENHL
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/db_xref="GI:21754301"
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/codon_start=1
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Williamson, A., Wheczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y.,
Wu, Y. P., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and
                                             Submitted (21-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jun 21, 2002 this sequence version replaced gi:21306532. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 46509)
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (03-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 46509)
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Direct Submission
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gc-help@bcm.tmc.edu
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JOURNAL REFERENCE

SITLE

TITLE JOURNAL AUTHORS

REFERENCE AUTHORS TITLE

JOURNAL

REFERENCE AUTHORS

JOURNAL TITLE

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are c sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing. only r of

# ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for annotation as region does not meet this standard, nnotation as Low Coverage. it will be indicated in the

repeat\_region

'rpt\_family="(CA)n"

family="(CA)n"

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot

FEATURES source repeat\_region misc\_feature repeat\_region /rpt\_family="MER33" | 11887. .120% complement (20236. /rpt\_family="MIR" complement (12070. /standard\_name="177147" complement(11575. .1187 /rpt\_family="7SK" 9534. .9793 complement (7906. complement (5816. complement (4564 complement (4330 complement (3471 complement (2988. complement (1968. complement (1661. complement (1457 complement (1240. complement (614. complement (321. complement (4.  $1871\overline{3}$ . 18116. 16886 \rpt\_ complement (3589 rpt\_family="AluSp" ndr. adt/ žůt 1dz/ jđ. db\_xref="taxon:9606" chromosome="3" organism="Homo sapiens" ocation/Qualifiers 1d. function="clone overlap" note="overlaps bases 182198. .184202 of clone AC008249" clone="RP11-268E23" rpt\_family="L2" family="L1MC4"
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AlaGluIleHisAsnGlnProGlnTrpGluThrHisLeuCysLysProValProGlnGlu 648
                                                                                                                     AlaAlaGlySerProProAlaProGly***MetSerLysHisArgGlyLysSerSerAla 608
                                                                                                                                                                               HisValGlnArgArgArgSerArgLeuLysGluProProGluLeuGlnSerSerGluArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCTTGCTCTTCATCATTTCACGGACTTATCCAATAACAACGACTTTTATATCCTA 23557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is undered the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus clone RP24-345H5,
AC119283
AC119283.1 GI:20304009
HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-APR-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren,B., Linton,L., Nusbaum,C.
Birsculus, clone RP24-345H5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                               Center clone name: 345_H_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
record is updated, the accession number will
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LOW-PASS SEQUENCE SAMPLING.
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27868: contig of 27968: gap of 28694: contig of 28794: gap of 29511: contig of 29611: gap of	23744: contig 23844: gap of 24571: gap of 24671: gap of 25283: contig 25483: gap of 26221: contig 26221: gap of 26221: gap of 26321: gap of	18803: contig of 18903: gap of 18903: gap of 19635: contig of 19735: gap of 20454: contig of 2054: gap of 21277: gap of 21377: gap of 22096: contig of 22196: gap of 22196: gap of 22194: contig of	277 12376: gap of 277 12376: gap of 137 1311: contig of 112 1321: gap of 212 13904: contig of 905 14004: gap of 905 14827: gap of 728 14827: gap of 828 15542: contig of 828 15542: contig of 643 15642: gap of 643 16456: gap of 643 17156: contig of 357 16456: gap of 17156: contig of 17779: contig of 17979: contig of	1551: contig 1651: gap of 2377: contig 2477: gap of 3204: contig 3304: gap of 4037: contig 4037: contig 4047: gap of 5677: contig 5677: gap of 6514: contig 6614: gap of 7343: contig 8177: gap of 8177: gap of 8179: gap of 10629: contig 9116: gap of 10629: contig 916: gap of 11629: gap of 11629: contig 1152: gap of 1152: gap of	contig of
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Timans, J.C., Debets, J.Eduard.Maria.Antonius., Sana, T.R.,
Bazan, J.Fernando. and Kastelein, R.A.
Human receptor proteins; related reagents and methods
Patent: US 6326472-A 3 04-DEC-2001;
Location/Qualifiers
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Sequence 3 from patent |
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8 8	. 40 136	AspGluproAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTy: 
음 성	60 196	ThralaHisSeralaGlyLeuThrLeuIleTrpTyrTrpThrargGlnAspArgAspLeu 
음 성	80 250	GluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeu
용 성	100 304	TrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThr        
용 성	120 . 364	ThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys
B &	138 424	PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly :::       :::::: TACAACAGCAGGATCCGCTATTTAGAAAAATCTGAAGTCACT
용 성	155 466	IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysPro 
용 왕	174 526	ThrIleThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnVallleProGlu 
8 8	194 586	GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal
용 성	214 646	ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal:::
음 성	234 694	ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisVal
용 성	253 754	ValTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPhe      ::: :::     -::
용 성	273 814	LeuMetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIl 
음 첫	293 859	thrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArg

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Homo sapiens interleukin-1 receptor 9 (IL1R9) mRNA,
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AF212016.1 GI:7363363
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Sana,T.R., Debets,R., Timans,J.C., Bazan,J.F. and Kastelein,R. Computational identification, cloning, and characterization of IL-IR9, a novel interleukin-1 receptor-like gene encoded over unusually large interval of human chromosome Xq22.2-q22.3 Genomics 69 (2), 252-262 (2000)
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DETNIDDNKEYDAYLSYTKVDQOTLDCDNFEEROPALFULFULFRHYGYKLFIPERDL
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                                                                                         CHVLDSAEQGLFGELQPIPSIAMTSTSATLVSSQADLPEFHPSDSMQIRHCCRGYKHE
                                                                                                                                                                                                                                                                                                                                                                                                                                       encoded by the sequence presented in Number AJ243874"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="transmembrane receptor type 1a; may signal NF-KB transcription factor; similar to IL1RAPL proencoded by the sequence presented in GenBank Acces
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role in immunity and development"
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/chromosome="X"
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Percent Similarity: Best Local Similarity:

2.63e-825.00 46.78% 31.93%

Length: Matches: Conservative: Mismatches:

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Score: Alignment Pred. No.:

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52 TGCAGAGGITATAAACATGAGATACCAGGCCACGACCTTGCCAGTACCTTCCTT	D <sub>D</sub>
7GluArgAlaAlaGlySerProProAlaProGly***MetSer 600	: <b>ઇ</b>
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17 GCAGAACAAGGACTTTTTGGAGAACTCCAGCCTATACCCTCTATTGCCATGACCAGTACT 17	문 .
48SerLeuSerAlaSerSerGlv 5	δ
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1597 CTGATCAAGTGGAAGGGATCCAAAAGCAGCAGCAAATTAAATTCTAAGTTTTGGAAGCACTTA 1656	망
521 PheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeu 540	Ş
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1375 GATCTCACAAGATATGTTGAACAAAGCAGAAGACTTATTATCGTGCTAACTCCAGACTAT 1434	Dр
453 AlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTyr 472	8
433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452	당 성
GACAATCCTGAAGAAGAGCAGTTTGCTCTTGAAGTACTGCCAGATGTCCTGGAAAAACAC 13	D
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/translation="MKPPFILALVCSVTSTNLKOVSKRNSVDGCIDMSVDLKTYMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(20. .101,102. .375,376. .562,563. .716,717. .791,792. .921,
922. .1067,1066. .1211,1212. .1382,1383. .2080)
/gene="ILTRAPL-2"
                                                                                                                                                                                                                             CTELKGKVNCQEVESLKRSIKLLSLIKWKGSKSSKLNSKFWKHLVYEMPIKKKEMLPR
                                                                                                                                                                                                                                                                NRNGRKHASVLLRKKDLIYKI BLAGGLGAI FLLLVLLVVIYKCYNI ELMLFYRQHFGA
DETNDDNKEYDAYLSYTKVDQDTLDCDNPEEEQFALEVLPDVLEKHYGYKLFIPERDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(1. .101,102. .375,376. .562,563. .716,717.
22. .1067,1068. .1211,1212. .1382,1383. .>2080)
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db_xref="taxon:9606"
                                                                                          evidence=experimental
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                                                         gene="IL1RAPL-2"
                                                                                                                number=2
                                                                                                                                  gene="IL1RAPL-2"
                                                                                                                                                                                           PATTLPVPSLGNHHTYCNLPLTLLNGQLPLNNTLKDTQEFHRNSSLLPLSSKELSFT
                                                                                                                                                                                                                                                PSGTYMEDLTRYVEQSRRLIIVLTPDYILRRGWSIFELESRLHNMLVSGEIKVILIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *>sue_type="adult brain"
.2080
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ORIGIN
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Best Local Similarity:
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                                                                                                                                        ThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSer-----Cys
                                                                                                                                                                                                                   TrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThr 119
                                                                                                                                                                                                                                                                                    GluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSer 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTGGATGGCTGATTGACTGGTCAGTGGAT----CTCAAGACATACATGGCTTTGGCA 154
                                                                       PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly-----
                                                                                                              TGGTTTCACTCAGCTGAGGCACAAGACAGTGGATTCTACACTTGTGTTTTAAGAAACTCA
                                                                                                                                                                                                                                                                  GAAGAGCCCATCATCTTT-----TCAGAGGTCAGGATGAGCAAAGAGGAAGATTCAATA
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Qy 493 IleAlaThrLysLeuIleValValGluTyrArgProLeuGluHisProHis 509	_
Db 1454 ATTCTCAGACGGGGATGGAGTATTTTCGAACTGGAAAGCAGACTCCATAACATG 1507	_
alThrGluLysSerIleSerMetLeuGlu 	_
Qy 453 AlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTyr 472 ::::::::::::::::        :::    :::	
Qy 433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 45 :::	
Qy 414AsnAlaGluGluGluGheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432	
OY 402 GIYLYSGIUTYTASPITETYFVAISETTYTALAARG	
382 TrpLeuGlumetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAsp 4   ::   :::::	_
Qy 362 CysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyr 381	
Qy 342 AlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeuAla 361	_ ^
Qy 322 ThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluVal 341	_ ^
Qy 313ThrGlnIleLeuSerIleLysLysVal 321	
Qy 293 ThrileAspValThrileAsnGluSerileSerHisSerArgThrGluAspGluThrArg 312	
Qy 273 LeuMetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIle 292 :::    :::    :::    :::    :::    Db 833 AGTGGAGAGTCTGGCCAATGATCTACTGGATGAAAGGAGAAAAAG	
253 ValTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPhe 272	
Qy 234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisVal 252	_
214	
Qy 194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213	
Qy 174 ThrileThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnVallleProGlu 193 :::        ::: Db 545 GATGTTGTGTGGTATAAGGAATGCAAGCCAAAAATGTGGAGAAGCATAATAATACAGAAA 604	
Db 485 AAAAGAAAGGAGATCTCCTGTCCAGACATGGATGACTTTAAAAAGTCCGATCAGGAGCCT 544	_

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PUBMED
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                   Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-1R) family. Delineation of a new class of IL-1R-related proteins based on signaling J. Biol. Chem. 275 (39), 29946-29954 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens TIGIRR-1 mRNA, complete cds. AF284436
                                                                                                                                                                                                                 Born,T.L., Smith,D.E., Garka,K.E., Renshaw,B.R., Bertles,J.S.Sims,J.E.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2212)
1 (bases 1 to 2712)
1 (carra K.E. Renshaw, B.R., Bertles, J.S. and
                                                                                                                                                             Submitted (05-JUL-2000) Molecular Biology, University St., Seattle, WA 98101-2936, USA
                                                                                                                                                                                                                                                                                                                                                                                         Born,T.L., Smith,D.E., Garka,K.E., Renshaw,B.R., Bertles,J.S. and
                                                                                                                                                                                                  Direct Submission
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US-10-061-727-2 (1-687) x AF284436 (1-2212)
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214 ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGlu
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                                                                                                                   GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
                                                                                                                                                                                              ThrileThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnVallleProGlu
                                                                                                                                                                                                                                                        AAAAGAAAGGAGATCTCCTGTCCAGACATGGATTTAAAAAAGTCCGATCAGGAGCCT
                                                                                                                                                                                                                                                                                            ---IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysPro
                                                                                                                                                                                                                                                                                                                                                                                          PheAsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly------
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                                                                                                                                                              GATGTTGTGTGTATAAGGAATGCAAGCCAAAAATGTGGAGAAGCATAATAATACAGAAG
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1808 GTATATGAAATGCCCATCAAGAAAAAAAGAAATGCTACCTCGGTGCCATGTTCTGGACTCC

1867

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1466 TATGGATATAAACTCTTCATCCCAGAAAGAGACCTGATTCCAAGTGGAACATACAT	ఠ
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	Db
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	Дb
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	Дb
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253 ValTyrGluLysGluProGlyGluGluLeuLleProCysThrValTyrPheSerPhe 272	Ş
845 ACAGCTTTACTCACAGACAAGCCTCCCAAGCCATTGTTCCCCATGGAGAATCAGCCAAGT 904	da.
234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisVal 252	ફ
797 CTTAAATATGAAGGAAAACTTGTAAGACGAACAACTGAATTGAAAGTT 844	DЬ

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Search completed: April 30, 2003, 11:50:48	2108 CTACCCCTTAATAACACCCTGAAAGATACCCCAGGAATTTCAC 2149	621 AsnHisLeuArgAsnLysSerArgAlaGluIleHis 632	2063 CACCATACTTATTGTAACCTGCCTCTGACGCTACTCAACGGACAG 2107	601 LysHisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGlu 620	2003 TGCAGAGGTTATAAACATGAGATACCAGCCACGACCTTGCCAGTACCTTCCTT	GluArgAlaAlaGlySerProProAlaProGly***MetSer 600	1961CCTGAATTCCACCCTTCAGATTCAATGCAAATCAGGCACTGT 2002	575 SerArgLeuLysGluProProGluLeuGlnSerSer	1928 TCAGCCACTCTGGTGTCATCTCAGGCTGATCTC 1960	555 TrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArgArg 574	1868 GCAGAACAAGGACTTTTTGGAGAACTCCAGCCTATACCCTCTATTGCCATGACCAGTACT 1927	SerLeuSerAlaSerSerGly 554

Search completed: April 30, 2003, 11:50:48 Job time : 3479 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1 MTLLWCVVSLYFYGILQSDA.....SALALHHFTDLSNNNDFYIL 687
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

Query

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Interleukin-18 rec	cDNA encoding a mu	Mouse interleukin-		DNA encoding trans	Mouse ST2L gene.	Murine interleukin	cDNA encoding a mo	Mouse interleukin-		ne interl	cDNA of clone GEMB	IL-1 re	cDNA of murine int		Human IL-18 recept			interlet	IL-1RD9	leukin				Interleukin-18 rec	cDNA encoding a hu	#18472 used	#14473 for	•	Ξ	٠.	_			Human II18D8 codi	Human TICIBB Codin			=			Mouse interleukin-	Human interleukin-	an	notation	7) } } [ 1   1   1   1   1   1   1   1   1   1

## ALIGNMENTS

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/*tag= a	CDS 101722	Key Location/Qualifiers		Homo sapiens.		IL-1; IL-1RI; ss; inflammatory response.	IL-1R acP; human; interleukin-1 receptor accessory protein; NF-kappaB;		Human interleukin-1 Receptor accessory protein (IL-1R acP) cDNA.		21-MAY-2002 (first entry)		AAS15608;		AAS15608 standard; cDNA; 1740 BP.	AAS15608	RESULT 1	ALIGNNENTS

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents the human interleukin-1 receptor accessory protein (IL-IRacP) cDNA of the invention. The interleukin receptor accessory protein (IL-IRacP) and its modulators (agonists) are useful for regulating cell function. Transient expression of either IL-IRac Palone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-IRI and IL-IRACP as a result of protein overexpression can elicit a signal transduction involving NF-kappaB activation. Modulation of signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity of IL-IRACP using binding agents such as agonists and antagonists. The IRACP as a consist and mutant IL-IRACP alleles in clinical and laboratory camples. Mutant alleles are used to generate allele-specific coligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In
                                                                                                                                                                                                                                                                                                                                                                                                                                              ed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1740 BP; 518 A; 360 C; 411 G; 451 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 active IL-1RAcP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1RacP) to a binding target.
                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 2; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function
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AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
                                                                                                                                                                          SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
                                                                         GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACA
                                                                                                       GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr 60
                                                                                                                                                      TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGAT
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ProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 10	0
CCAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGG 30	9
01 PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 12	0
21 TyrCygSerLygValAlaPheProLeuGluValValGlnLygAgpSerCygPheAgnSer 14	0 1
0 TATTGCAGCAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC 42	9
1 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 16	0
1 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 18	0
CAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGG 54	9
ysTyrLysIleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeuSerPheLeu 20	0
GTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTC 60	9
01 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 22 	9 0
rgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 24	0
GTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGGT	9
alProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 26	0
30 GTGCCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAA	9
1 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 28 	9 0
rpfirpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 30	0
GGTGGACCATTGATGGAAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA 90	9
erIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 32	0
GTATAAGTCATAGTAGAACAGAAGAACAAGAACTCAGATTTTGAGCATCAAGAAA 96	9
21 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 34 	0 29
41 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu 36	0
TTGCCAAAGCAGCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTG 10	99
61 AlaCysGlyPheGlyAlaThrValLeuLeuVallVallleLeuIleVallValTyrHisVal 38	6
81 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 40	99
spGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluGluGluPhe 42	0
10 GATGGAAAAGAGTATGATATTTATGTATCCTATGCAAGGAATGCCGGAAGAAGAAGAATTT 12	9
1 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 44	š
	81 GlubrolleAssipheArgiculProGluAssiArgileScritysGlutysAspValleuTrp 10.1 PheArgiculProCoccicoccadaAccoccatingTrincysMacgacaticTrince 10.1 PheArgiculProCoccicoccadaAccoccatingTrincysMacgacaticTrince 10.1 PheArgiculProCoccicoccacaticCoccadaAccoccatingTrincysMacgacaticTrince 10.1 PheArgiculProCoccicoccacicTricoccacaticAccicocatingTrincysMacgacaticTrince 10.1 PheArgiculProCoccicocacaticAccicocatingTrincysMacgacaticTrince 10.1 PheArgiculProCoccicocacicTricocacatingTrincysMacgacaticTrince 10.1 PheArgiculProCoccicocacicTricocacatingTrincysMacgacaticTricocaccatingTrince 10.1 PheArgiculProCoccicocacicTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacaticTricocacatingTrincysMacgacatingTrincy

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                                                 Isolated interleukin-1 receptor accessory protein - used to develop prods. to treat or prevent inflammatory or immunological activities of interleukin-1
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A cDNA clone (AAT32026) codes for human interleukin-1 receptor accessory protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind to or otherwise activate the IL-1R,
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GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT
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Percent Similarity:
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                                         ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys
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                                                                                                        CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA
                                                                                                                          ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla
                                                                                                                                                                    ATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGA
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                                           Mouse interleukin-1 receptor accessory protein cDNA.
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ACGGTGCTCACGGTCATTAAATGGAAAGGGGAAAAATCCAAGTATCCACAGGGCAGGTTC 161
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                                                                                                                                                                                                                                                                                 TrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSerGlyTrpAsn 556
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receptor accessory protein;
therapy; antiinflammatory;
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             antagonist;
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accessory protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind to, or otherwise activate, the IL-1R, esp. the Type 1 IL-1R. It was obtd. by screening cell-surface proteins in COS-7 cells transfected by 3T3-L1 cDNA using anti-murine IL-1R AcP monoclonal antibody 4C5, and isolation of cDNA clones from positive lines. The murine cDNA was used to obtain a partial genomic clone of the human homologue. A probe derived from this genomic clone was then used to isolate the full-length cDNA (AAT32026) for human IL-1R AcP (AAW01911).
                                                                                                                                                                                                          Isolated interleukin-1 receptor accessory protein - used to develop
prods. to treat or prevent inflammatory or immunological activities
of interleukin-1
                                                                                                                             A cDNA clone (AAT32028) codes for mouse interleukin-1 receptor accessory protein (IL-1R AcP), a protein that inhibits the
                                                                                                                                                                                                                                                                                                                      Chizzonite RA,
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DB; AAW01913.
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Percent Similarity: Best Local Similarity: Query Score: Match: Scores: 9.17e-192 2327.50 87.61% 75.93% 63.44% Matches: Conservative: Mismatches: Indels: ength: 1713 429 66 55 15

Sequence 1713 BP; 473 A; 386 C;

428 G; 426 T; 0 other;

US-10-061-727-2 (1-687) x AAT32028 (1-1713)

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| GAGCCGGCTCGAATCAAGTGCCCCCTCTTTGAACACTTCCTGAAGTACAACTACAGCACT
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SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet
                               AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg
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        This sequence represents the mouse interleukin-1 receptor accessory protein (IL-IR AcP) CDNA that was used to generate a CDNA fragment used as a hybridisation probe to isolate, from a CDNA library, the human IL-IR AcP CDNA of the invention. The interleukin receptor accessory protein (IL-IR AcP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-IRI or IL-IRACP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in
                                                                                                                                                                                                          WPI; 200
P-PSDB;
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IL-1;
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                                                                                                                                           Example;
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DB; AAU09967.
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IL-1RI; ss;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ry Match:
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                                                                                                                        CysTyrLysIleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeuSerPheLeu 200
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                                                    IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly
                                                                                                                                                                                                                                                                                                                   TACTGCAGCAAAGTTGCATTTCCCCCTGGAAGTTGTTCAGAAGGACAGCTGTTTCAATTCT
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 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla
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luProProGluLeuGlnSerSerGluArgAlaAlaGlySer 592	Pro	Ą
CAATGACAAGCAGGG-TCTCTCCTACTCATCCCTGAAAA	AGCA	Дb
rSerGlnSerAspIleSerLeuAspHisValGlnArg 	SerCysSerS	Ş
sAlaLeuArgLeuAlaLeuProLeuArgSerLeuSerAlaSerSer 553 	534 SerLysPheTrpLysAlaLeuArgLev :::         1740 GGCAGGTTCTGGAAGCAGTTGCAGGTV	B &
erPheValSerTrpLysGlyGluLysSerLysHisSerGly 53 :: ::                :: CGTCATTAAATGGAAAGGAGAGAAATCCAAGTATCCTCAG 17	517 GluSerValSerPheVa: ::: 1680 CGGGCTAAGACGGTGCTCACGGTCAT	당 <i>Q</i>
yrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys 516 		B 8
alMetCysGlnAsnSerIleAlaTh :::::::   :: TAGAAAATATGGCCTC	: 5	B 8
.euSerProAspTyrValThrGluLysSe         :::       TAAGTCCCAACTACGTGCTCCAGGGAAC	461 SerargargMetIlevalValLeuSe:	g Q
roGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 460          :::               :::	441 AspArgAspSerLeuProGlyGlyAsi	g Q
rgGlyValLeuGluAsmGluPheGlyTyrLysLeuCysIlePhe 440 	421 ValleuLeuThrLeuArgGlyValLeu 	D Q
SplleTyrValSerTyrAlaArgAsnAlaGluGluGluGluPhe 420 	401 AspGlyLysGluTyrAspIleTyrValSe 	B 8
alleuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400 	381 TyrTrpLeuGluMetValleuPheTyr 	B 8
GlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380                    	61 Alacys	D Q
ysValLysGlnLysValProAlaProArgTyrThrValGluLeu 360                 	341 ValAlaLysAlaAlaLysValLysGlr :::               1155 GCTGAGCAGGCTGCCAAGGTGAAACA	D Q
eulysargSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340    :::   :::               ::   CAGGCGAACTATGTCTGTCATGCTCGAAATACCAAAGGGGAA 1154	321 ValThrSerGluAspLeuLysArgSer	g 4g
rArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 320 	301 SerIleSerHisSerArgThrGluAsp	B &
YLYSLYSProAspAspIleThrIleAspValThrIleAsnGlu 300                   		B &
SThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280	ThrValTy	B &
ssSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260 ::           aTTCTCCAAATGACCGTGTTGTCTATGAGAAAGAACCAGGAGAG 914	ProAs CCAA	Db .
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                                                  US-10-061-727-2 (1-687) x AAT32027
                                                                             Query Match:
DB:
                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                             Pred. No.:
                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                        human interleukin-1 receptor accessory protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind to, or otherwise activate IL-1R, esp. the Type 1 IL-1R. It was obtd. by PCR amplification (see also AAT32029-30) of cDNA (AAT32026) coding for the extracellular domain of IL-1R AcP (AAM01911). The soluble protein was expressed in Sf9 insect cells using a baculovirus system. It can be used to treat or prevent the inflammatory or immunological activities of IL-1, and also to screen for IL-1 antagonists.
                                                                                                                                                                                                                                                                                                                                                                       Isolated interleukin-1 receptor accessory protein - used to develop
prods. to treat or prevent inflammatory or immunological activities
of interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-362691/36.
P-PSDB; AAW01912.
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inflammation; therapy; antiinflammatory; ss.
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                                                                                                                                                                                  Sequence 1077 BP; 326 A; 234 C;
                                                                                                                                                                                                                                                                                                                    A cDNA clone (AAT32027) codes for a soluble form (AAW01912) of the
                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 80-81; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chizzonite RA, Ju GW;
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ProProAla-ProGly***MetSerLysHisArgGlyLysSerSer 607
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                                                                                     Conservative: Mismatches: Indels:
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RESULT 6 AAA09048 ID AAA09048 standard; DNA; 2733 BP. XX	Qy 341 ValAlaLysAlaAlaLysValLysGlnLys	ω ω	Qy 301 SerIleSerHisSerArgThrGluAspGluThr/	Qy 281 TrpTrpThrIleAspGlyLysLysProAspAs	Qy 261 GluLeuLeuIleProCysThrValTyrPheS	Qy 241 ValProProValIleHisSerProAsnAspHisVa	21 ArgThrPheHisLeuTh	201 IleAlaLeuIleSerAsnAsnGlyAsnTy	181 CysTyrLysIleGlnAsnPheAsnAsnVa 	161 ProAsnValAspGlyTyrPheProS	<u>ч</u> 4.	Qy 121 TyrCysSerLysValAlaPheProLeuGluValValQ	101 PheArgProThrLeuLeuAsnAsp	Qy 81 GluProIleAsnPheArgLeuProGluAsnArgl	Qy 61 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAs 	Qy 41 GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSe 	
	AlaProArgTyrThrValGlu 359          GCTCCAAGATACACAGTGGAA 1077	HisAlaArgSerAlaLysGlyGlu 340                        CATGCTAGAAGTGCCAAAGGCGAA 1020	ThrGlnIleLeuSerIleLySLyS 320 	eThrIleAspValThrIleAsnGlu 300 	SerPheLeumetAspSerArgAsnGluVal 280 	ValValTyrGluLysGluProGlyGlu 260 	rArgThrLeuThrValLysValValGlySerProLysAsnAla 240 	rThrCysValValThrTyrProGluAsnGly 220 	ProGluGlyMetAsnLeuSerPheLeu 200 	ProThrIleThrTrpTyrMetGly 180 	uTyrGlylleGlnArglleFhrCys 160            ATATGGCATTCAGAGGATCACTTGT 480	GlnLysAspSerCysPheAsnSer 140                       CAAAAAGACAGCTGTTTCAATTCC 420	ThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120 	IleSerLysGluLysAspValLeuTrp	ThràrgGlnAspArgAspLeuGlu 80              CTAGGCAGGACCGGGACCTTGAG 240	PheLeuLysPheAsnTyrSerThr 60 	CATGAGGCAAATCCAAGTGTTTGAAGAT 120

AAA09048;

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                                                                                                                                                                                                                                                                           cytokine by binding the cytokien to form a non-functional complex. The creeptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in the presence of a ligand, a non-functional intermediate complex, consisting of the ligand, its alpha recepotr and its beta-1 receptor component, can be formed, it will effectively block the action of the ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers of the extracellular domains of the alpha specificity determining components of their receptors and the extracellular domain of gpl30. The resultant heterodimers, function as high-affinity traps, rendering the cytokine inaccessbile to form a signal transducing complex with the native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or
                                                                                                                                                                                                                                                                                                                                                                    signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to form heterodimers (sR-alpha:beta-1) that act as antagonist to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes fusion polypeptide 569, which is capable of binding cytokine IL-1 to form a non-functional complex. The invention concerns production non-functional complex any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to form a nonfunctional complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule for treating cytokine-related diseases or disorders encodes a fusion polypeptide capable of binding a cytokine
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19-MAY-1999;
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                                                          disorders such as
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                                    including
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; immunomodulator;
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99US-0313942.
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                                      s osteoporosis and primary and secondary multiple myeloma or cachexia.
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Percent Similarity:
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Query Match:
DB:

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Length: Matches: Conservative: Mismatches: Indels:

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                                                                 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu
                                                                                                                      SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys
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RESULT 7
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Percent Similarity:
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Pred. No.:
                                                                                               This cDNA clone codes for human interleukin-1 receptor accessory molecule (II1-R AcM) (see AAW53897), a new member of the immunoglobulin superfamily that forms a complex with type 1 II1-R and which has higher affinity for II-1 than the receptor itself, suggesting that the known high and low affinity forms of II1-R are in fact the receptor with or without II1-R AcM, respectively. The 2155 bp sequence is present in clone HMEEJ52 (deposited as ATCC 97666) derived from microvascular epithelium (no details of ATCC 97666) derived from microvascular epithelium (no details of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                    and recombinant vectors are claimed. Also claimed are isolated nucleic acid molecules encoding epitope-bearing portions (see AAW53898-915) of III-R ACM. Recombinant III-R ACM can be used to identify II-IR agonists and antagonists useful for therapeutic modulation of II-1 activity, and to raise specific antibodies. Nucleic acid fragments are useful as diagnostic probes and primers for isolation of III-R ACM-encoding genomic sequences, for in situ hybridisation to determine chromosomal localisation of the gene, for chromosome identification and for identifying mutations that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding interleukin-1 receptor accessory used for therapeutic modulation of IL-1 activity
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signal transduction; infection; septic shock; inflammation;
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                                                                                                                                                                                                                                                                 isolation given). Recombinant expression in Escherichia coli, mammalian and insect cells is described. Recombinant host cells
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                                                                                                                   GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal
                                                                                                                                            ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys
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TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu
                                                                                                          CAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT
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                                                                                                                                                                                          ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide, designated IL-1 receptor DNAX designation 8 (IL-1RDB), of the invention. The IL-1RDB, IL-1RDB, and IL-1RDD proteins, their fragments and mutchs, also related antibodies, other binding agents and (ant) agonists are used to treat conditions associated with abnormal expression of the polypeptide or abnormal expression of, or response to, their ligands, e.g. immunological, inflammatory or morphological disorders. They may also be used to screen for binding agents (potential drugs), diagnostic reagents (to detect the proteins or their ligands) and to isolate related sequences. Antibodies may also be used to raise anti-idiotypic antibodies, as carriers for toxins, radionuclides or other therapeutic agents, and for affinity purification.
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12-MAR-1998;
18-MAR-1998;
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IL-1 receptor-like
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15-APR-1998;
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IL-1RD8
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immunological disorder; ds.
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mammalian physiology such as morphogenesis of immune system function. The invention particularly relates to nucleic acids, proteins and antibodies which regulate development and/or the immune system. The invention also relates to antibody fragments which specifically bind to antigenic fragments of a primate interleukin (II)-1 receptor like molecules such as II-1 receptor DNAX designation (II-1RD). The antibody fragments of the invention are useful to treat conditions exhibiting abnormal expression of the receptors or their ligands which typically will be immunological disorders. The present sequence is a DNA encoding Disclosure; Antibody fragments which specifically bind to primate interleukin receptor-like molecules are useful to treat conditions associated abnormal expression of the receptor or its ligand, particularly immunological disorders -The present invention relates to compositions Column 11-16; 102pp; English. and methods for affecting with

2002-121110/16.

AAE16567.

Sequence 2061 BP; 656 A; 421 C; 459 e. 525 T; 0 other;

human IL-1RD8

Alignment Scores:			
Pred. No.:	1.9e-61	Length:	2061
Score:	825.00	Matches:	228
Percent Similarity:	46.78%	Conservative:	106
Best Local Similarity:	31.93%	Mismatches:	244
Query Match:	22.49%	Indels:	136
DB:	24	Gaps:	27

US-10-061-727-2 (1-687) x AAD27170 (1-2061)

- 밁 8 밁 Ś 79 19 MetThrLeuLeuTrpCys---ValValSerLeuTyrPheTyrGlyIleLeuGlnSerAsp 19 TCTGTGGATGGCTGCATTGACTGGTCAGTGGAT---CTCAAGACATACATGGCTTTGGCA 135 AlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGlu TTGGCCCTTGTGGTCTGTTCTGTAGTCAGCACAAATCTGAAGATGGTGTCAAAGAGAAAT 39 78
- 40  ${\tt AspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSer}$

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luMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAsp 4	5
362 CysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyr 381	B 8
342 AlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeuAla 361	B 8
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94 ACAGCTTTACTCACAGACAAGCCTCCCAAGCCATTGTTCCCCATGGAGAATCAGCCAAGT	₽ ₽
34 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisVal 2	<b>\$</b> .
214 ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 233 :::	문 성
194 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213	용 성
174 ThrileThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnVallleProGlu 193 :::            :: 526 GATGTTGTGTGGGTATAAGGAATGCAAAGCCAAAAATGTGGAGAAGCATAATAATACAGAAA 585	B 8
ο σ	뮹 :
138 PheAsmSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154 :::      ::::	; <b>8</b>
120 ThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCys 137	용 성
100 TrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThr 119	유 성
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60 ThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeu 79	용 왕
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TIGIRR; human; chromosome X; FG syndrome; premature ovarian failure-1;

Human TIGIRR coding sequence.

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RESULT 10
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Alignment
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                                                                                                                                               US-10-061-727-2 (1-687)
                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                            TIGIRR polypeptide counter-structures; (v) as molecular weight markers electrophoresis; (vi) for determining isoelectric points of unknown proteins; (vii) as controls for determining the extent of protein fragmentation (e.g. to aid characterisation of protein structures by maspectrometry); (viii) for generation of antibodies (Ab); and (ix) to deliver diagnostic or therapeutic agents to cells that express TIGIRR, binding molecules. Ab are used for affinity purification of TIGIRR; therapeutically to inhibit binding of TIGIRR to its counter structures, and (if agonistic) to promote cell signalling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (b) to identify human chromosome X, to map genes on this chromosome and to identify disease-related genes (particularly in the region Xq21.3-22 where genes are present associated with e.g. FG syndrome, premature ovarian failure-1, leiomyomatosis, epilepsy, Bazex syndrome etc.) including detection of defective genes; (c) to study cell-signal transduction and the TIGIRR system, and (d) in gene therapy. Sense and antisense oligonucleotides derived from the TIGIRR coding sequence can be used to inhibit expression of the TIGIRR Gene. The TIGIRR protein, or its soluble fragments, are used: (i) to study cellular processes (immune regulation, proliferation, death, migration, interaction with other cells and inflammation); (ii) to identify and purify proteins that associate with TIGIRR policials and inflammation).
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                                                                                                                                                                                                                                                                                                                               Sequence 1979
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                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with TIGIRR ligands and receptors, and to measure their biological activity; (iii) in screening for, and rational design of, potential inhibitors of activity; (iv) therapeutically against diseases mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence encodes the human TIGIRR protein of the invention. The TIGIRR DNA sequences can be used: (a) as probes or primers for identifying nucleic acid that encodes proteins with TIGIRR activity.
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                     ArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSer 63
                                                                      TGCATTGACTGGTCAGTGGAT---CTCAAGACATACATGGCTTTGGCAGGTGAACCAGTC 65
                                                                                               CysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluProAla
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                                                                                                                                                                                                             AACACCCTGAAAGATACCCAGGAATTTĆAC
                                                                                                                                                                                                                                                                                             LysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGluAsnHisLeuArg 624
                                                                                                                                                                                                                                                                                                                                                                                                               GluProProGluLeuGlnSerSer------
                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGTCATCTCAGGCTGATCTC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGGATCCAAAAGCAGCAAATTAAATTCTAAGTTTTGGAAGCACTTAGTATATGAAATG
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                                                                                                                                                                                                                                       Asn-----LysSerArgAlaGluIleHis 632
                                                                                                                                                                                                                                                                  -----ACTTATTGTAACCTGCCTCTGACGCTACTCAACGGACAGCTACCCCTTAAT 1886
                                                                                                                                                                                                                                                                                                                          CysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArgArgSerArgLeuLys
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                                                                                                                                                      standard; cDNA; 1737 BP.
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        IRD8; IL-IRD10; interleukin-1; IL-Ireceptor DNAX; therapy; r-like protein; abnormal expression; immunological disorder; disorder; morphological disorder; ss.
                                                                                            (first entry)
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                                                                 sequence.
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Alignment Scores:
                                                    This sequence encodes a interleukin-1 (IL-1) receptor-like polypeptide, designated IL-1 receptor DNAX designation 8 (IL-IRD8), of the invention. The IL-IRD8, IL-IRD9, and IL-IRD10 proteins, their fragments and muteins, also related antibodies, other binding agents and (ant) agonists are used to treat conditions associated with abnormal expression of the polypeptide or abnormal expression of, or response to, their ligands, e.g. immunological, inflammatory or morphological disorders. They may also be used to screen for binding agents (potential drugs), diagnostic reagents (to detect the proteins or their ligands) and to isolate related sequences. Antibodies may also be used to raise anti-idiotypic antibodies, as carriers for toxins, radionuclides or other therapeutic agents, and for affinity purification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-AUG-1998;
15-OCT-1997;
17-NOV-1997;
                             Sequence 1737 BP; 566 A; 330 C; 397 G; 444 T;
                                                                                                                                                                                                                                                                                 Interleukin-1 receptor-like polypeptides RD8,
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                                                                                                                                                                                                                                                                                                                                             Bazan
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98US-0040714.
98US-0081883.
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                             0 other;
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Pred. Score: Percen Best I Query DB:	Pred. No.:  2.17e-59 Score:  800.00 Percent Similarity:  51.44 Best Local Similarity:  35.14 Query Match:  21.80 DB:	Length: Matches: Conservative: Mismatches: Indels: Gaps:	1737 207 96 208 208 78	
us-10	US-10-061-727-2 (1-687) x AAX58247 (1-1737)	8247 (1-1737)		
Ş	1 MetThrLeuLeuTrpCysVa	MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAsp	leLeuGlnSerAsp	19
DЬ	7 CTCACACTATTAGI	CTCACACTATTAGTGTCAACAATGCTCACTGTATCCTTATACCTCTTCTGATTTT 60	ATACCICITCIGATITI	0
Ś	20AlaSerGluArgCysAs	20AlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPhe 38	rgGlnIleGlnValPhe	38
DЪ	61 CITTCAGTGGATGGCTGCAT	61 CTTTCAGTGGATGGCTGCATTGACTGGTCAGTTGGATCTCAAGACATACATGGCTTTG 117	AGACATACATGGCTTTG	117
Ş	39 GluAspGluProAlaArgIl	GluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyr		58
Db	118 GCAGGTGAACCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTTCGTACCAACTAT 177	GAAATGTGCCCTTTTCTACAGTT	ATATTCGTACCAACTAT	177
Ş	59 SerThrAlaHisSerAlaGl	YLeuThrLeuIleTrpTyrTrpT	hrArgGlnAspArgAsp	78
Db	178 AGCACGGCCCAGAGCACTGG	AGCACGGCCCAGAGCACTGGGCTCAGGCTTATGTGGTACAAAAAACAAAGGTGAT 231	AAAAACAAAGGTGAT	231
Ş	79 LeuGluGluProIleAsnPh	LeuGluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspVal 98	erLysGluLysAspVal	8
ДЪ	232 TIGGAAGAGCCCATCATCTT	TTGGAAGAGCCCATCATCTTTTCAGAGGTCAGGATGAGCAAAGAGGAAGATTCA 285	GCAAAGAGGAAGATTCA	285
Ş	99 LeuTrpPheArgProThrLe	LeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsn 118	hrCysMetLeuArgAsn	118
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ACTAAAAGAAAGGAGATCTCCTGTCCAGACATGACTTTAAAAAAGTCCGATCAGGAG
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                                                                                                                                                                                                                                                                             AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
                                                                                                                                                                                                                                                                                                                                ---- AAACATGCCAGTGTTTTGCTGCGTAAAAGGATTTAATCTATAAAATTGAGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAGTGGAGAGTCTGGGCCAATGATCTACTGG---ATGAAAGGAGAAAAG-----
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                    GluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThr---
                                                              GACAACAAGGAATATGATGCTTATCTCTTTACACAAAAGTGGACCAAGATACTTTAGAC
                                                                                                                                                      AspGlyLysGluTyrAspIleTyrValSerTyrAlaArg-----
                                                                                                                                                                                                TACAACATTGAATTGATGCTCTTCTACAGGCAGCACTTTGGAGCTGATGAAACTAATGAT 1176
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                      Antibody fragments which specifically bind to primate interleukin receptor-like molecules are useful to treat conditions associated abnormal expression of the receptor or its ligand, particularly immunological disorders -
                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                 Human interleukin-1 receptor
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      Disclosure; Column 7-10; 102pp; English
                                                                 P-PSDB; AAE16566.
                                                                          WPI; 2002-121110/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProHisProGly---
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                                                                                                                                                                                                                                                                                                                     morphogenesis; immune system; interleukin-1 DNAX designation
8 protein; therapy; immunological disorder; ds.
                                                                                           JC,
                                                                                                            SCHERING CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerPheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLys
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97US-065776P.
98US-078008P.
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                                                                                                                                                                                                                                          /*tag= a.
/product= "Human IL-1RD8 protein"
/note= "CDS does not include start
/partial
                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
                                                                                           JEMA,
                                                                                                                                      3-078416P.
3-081883P.
                                                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                             Bazan
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to compositions and methods for affecting mammalian physiology such as morphogenesis of immune system function. The invention particularly relates to nucleic acids, proteins and antibodies which regulate development and/or the immune system. The invention also relates to antibody fragments which specifically bind to antigenic fragments of a primate interleukin (IL)-1 receptor like molecules such as IL-1 receptor DNAX designation (IL-IRD). The antibody fragments of the invention are useful to treat conditions exhibiting abnormal expression of the receptors or their ligands which typically will be immunological disorders. The present sequence is a DNA encoding human II-IRD8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1737 BP; 566 A; 330 C; 397 G; 444 T; 0 other;
                                                                                                                                                                                                                                                                                                                             155 -----IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLys 172
::: |||:::||| :::
448 ACTAAAAGAAAGGAGATCTCCCTGTCCAGACATGGATGACTTTAAAAAGTCCGATCAGGAG 507
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                                                       628 GAACTTAAATAT-
                                                                                                                                                                                   193 GluGlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCys
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ValValGlySerProLysAsnAlaValPro---ProValIleHisSerProAsnAspHis 251
                                                                                  ValValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLys
                                                                                                                                                                                                                                                                             ProThrIleThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValllePro 192
                                                                                                                                            AAAGGAAATGCTCTTCTGATCCAAGAAGTTCAAGAAGAAGATGGAGGAAATTACACATGT
                                                                                                                                                                                                                                   CCTGATGTTGTGGTÄTAAGGAATGCAAGCCAAAAATGTGGAGAAGCATAATAATACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuTrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsn 118 :::||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGAAGAGCCCATCATCTTT-----TCAGAGGTCAGGATGAGCAAAGAGGAAGATTCA 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCACGGCCCAGAGCACTGGGCTCAGGCTTATGTGGTAC-----AAAAACAAAGGTGAT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAsp 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluAspGluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyr 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTTCAGTGGATGGCTGCATTGACTGGTCAGTGGAT---CTCAAGACATACATGGCTTTG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---AlaSerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPhe 38
                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTACAACAGCAGGATCCGC------TATTTAGAAAAAATCTGAAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCAGGTGAACCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCACACTATTA-----GTGTCAACAATGCTCACTGTATCTTATACCTCTTCTGATTTT
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RESULT 13 AAA27919

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3 538 1 163	520SerPheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLys	용 성
- 519 r 157	508 ProHisProGly	용 성
8 507 - 152	491 ASnSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHis     :::         :::           ::: 1471 AACATGCTAGTCAGTGGAGAAATCAAAGTGATTTTGATTGA	음 성
n 490 T 147	471 AspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln	B 5
o 470     A 1416	451 ValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerPro :::    :::     :::	용 성
- 450 C 135	432 GluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThr :::	유 성
<u>م</u> ب	414AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsn	음 성
- 413 C 123	401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArg	용 성
u 400 T 117	381 TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 	B 8
1 380 C 111	361 AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal	B 8
ü 360   T 105	341 ValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeu	음 성
и 340 ю 1002	321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu	B 8
's 320 'A 945	312 ArgThrGlnIleLeuSerIleLysLy	음 성
r 311 A 885	292 IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThr	유 성
3p 291 843	272 PheLeuMetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAs	용 성
er 271 EA 795	252 ValValTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSer	g 9
ъ 735	 	Дb

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Pred. No.:
Score:
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                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                               that is encoded by a gene on the X chromosome. The sequence was cobtained by high-throughput sequencing of chromosome region Xp11, PCR and 5' RACE reactions. The invention is directed to novel, purified and isolated II-1 zeta, II-1 zeta splice variants and Xrec2 polypeptides (see AAY25297-301), the nucleic acids (see AAA27918-22) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. Xrec2 nucleic acids are used to: to express Xrec2 polypeptides; as probes to identify nucleic acids encoding proteins of the II-1 receptor family; to identify numan chromosome X; to map genes on chromosome X; to identify genes associated with diseases, syndromes, or other conditions associated with chromosome X; such as retinoschisis, lissencephaly, subcortical laminalheteropia, mental retardation, cowchock syndrome, bazex syndrome, hypertrichosis, lymphoproliferative syndrome and immunodeficiency; as single-stranded sense or antisense oligonucleotides to inhibit expression of Xrec2 polypeptides; to help detect defective genes in an individual; and for gene therapy.
                                                                                                                                                                                  Sequence 2091 BP; 644 A; 432 C; 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12(a); Page 8-9; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-442387/38.
P-PSDB; AAY95298.
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retinoschisis; lissencephaly; subcortical laminalheteropia;
mental retardation; chowchock syndrome; bazex syndrome;
hypertrichosis; lymphoproliferative syndrome; immunodeficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of the coding region of cDNA encoding human Xrec2, a member of the interleukin-1 (IL-1) receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for identifying genes associated with diseases such as glaucoma, and insulin-dependent diabetes mellitus
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10-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA27919 standard; cDNA; 2091 BP
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99US-0164675.
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47.33%
29.35%
21.04%
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                                                                       Mismatches:
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1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla 20
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366 109	ValLysGlnLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAla	347	g &	
103	GGAAATTACTCCTGTTATGTTGAAAATGGAAATGGAACGTCGACACGCCAGC	988	ф	
346	LysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLys	327	ঠ	
326 987	ThrGluAspGluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu	307 931	B 8	
930	GATGAAAATCGAGTTTGGGAAAGTGACATTAGAATTCTTAAGGAGCATCTT	880	B	
306	ThrIleAspValThrIleAsnGluSerIleSerHisSerArg	293	ઇ	
879	AGCGGAGATGTCAGTCCTTTAATTTACTGGATGAAAGGAGAAAAATTTATTGAAGATCTG	820	뫄	
292	LeuMetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIle	273	Ş	
819	ATTCAGGAGACCCAGCTGGGTGACCTCGCTAATCTAACCTGCAGAGCTTTCTTT	760	문 5	
373	GCCCCTCTGACTGATAAGCCCACCCAAGCTTTTGTATCCTATGGAAAGTAAACTGACA	703	? ;	
252	GlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisVal	235	8	
702	AAATATGGAGGCTTTGTTGTGAGAAGAACTACTGAATTAACTGTTACA	655	В	
234	ThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValVal	215	ર્ક	
654	GATACTCTGCTTATAAGAGAAGTCAGAGAGATGACATTGGAAATTATACCTGTGAATTA	595	망	
214	MetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValVal	195	Ş	
594	ATCCTTTGGTACAAGGAATGCAGGACAAAAACATGGAGGCCAAGTATTGTATTCAAAAGA	535	뫄	
194	<pre>IleThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGly</pre>	175	Ş.	
534	AGCAAGGAAATTTCATGCCGTGACATAGAGGATTTTCTACTGCCAACCAGAGAACCTGAA	475	망	
174	<pre>IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr</pre>	155	ઇ	
474	ATTCCAAGATGAAGTATTTTGAAAAAGCTGAACTTAGCAAA	433	뮍	
154		139	S	
432	TACTGTATGAAAGTATCCATCTCACTGACAGTGGGTGAAAATGACACTGGACTCTGCTAT	373	B 2	
	IICCGGCCAACAIIGCIACAGGAACAGIGGICICIACGCCIGIGICAICAGAAAACICAGA	, i	9 5	
120	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	101	\$ 8	
312	GAGCCAATAGCCTTTGACGGAAGTAGAATGAGCAAAGAAGAAGACTCCATTTGG	259	뮍	
100	GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp	81	8	
258	GCCCAAAGTGCTGGACTCAGTTTGATGTGGTACAAAAGTTCTGGTCCTGGAGACTTTGAA	199	В	
80	AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu	61	8	
198	GAGCCTGTTCGAATCAAATGTGCACTCTTTTATGGTTATATCAGAACAAATTACTCCCTT	139	뫄	
60	GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr	41	S	
138	GCCGATGGATGCACTGGTCTATCGATATCAAGAAATATCAAGTTTTGGTGGGA	82	문	
40	SerGluArgCYsAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp	21	Ş	
81	${\tt TTGATTCTCTTATACGCTACTTTTACTCAGAGTTTGAAGGTTGTGACCAAAAGAGGCTCC}$	. 22	рь	

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                                                                                                                                                                         GlyGlu-AsnHisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGl
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                                                                                                                                            GGGCAGCGGCCACAGACAAAATCGAGCAGGGAGCAGAATCCAGATGAGGCCCACACAAAC 2034
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Percent Similarity:
Best Local Similarity:
                                                                                                                    US-10-061-727-2 (1-687)
                                Query Match:
                                                                                            Alignment Scores:
                                                                                                                                                                                      The invention relates to polymucleotides (AAKS1456-AAKS3435) and the encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, inmunomodulatory activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                      Claim 1; Page 1748-1752; 6221pp; English
                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-476283/51.
P-PSDB; AAM78808.
                                                                                                                  Sequence 3122
                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages
                                                                                                                                                                                                                                                                                                                                                                                                                       Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000;
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20-JUN-2000;
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Wang D,
Yang Y,
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2000US-0598075

2000US-0620325

2000US-0654936

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2000US-0728422
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, Wang J, Zh
Wejhrman T,
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T, Goodrich J
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1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla

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AGTGCCATCCTGCCGCTG-TTGCCAAGGGAGACCAGTATATCCAGTGTGATATGGTGACA 2603	2545 AGTGCCATCCTGCCGCTG-TTGCCAAGGGAC	B &
	85	B
GlyGlu-AsnHisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGl 638	619 GlyGlu-AsnHisLeuArgAsnLysSerArg	Ş
GCATACCTACTGTAACATCCCTATGACACTCATCAAC 2484	2425 CCTCTTACCTCCATAGGCAATCAGCATACCT	В
MetSerLysHisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGlu 618	599 MetSerLysHisArgGlyLysSerSerAla	ঠ
TITION TO THE TITION TO THE TRANSPORT TO	2371 CAGAAACACTACTACCGAAGCTATGAGTACGACGTA-	B
lySer	579 GluProProGluLeuGlnSerSerGluArg	8
GCCACTGCCCATCCAGATCTCCGTTCTACCTTTCACAACACGTACCATTCACAAATGCGT 2370	2311 GCCACTGCCCATCCAGATCTCCGTTCTACC	Db
gArgSerArgLeuLys 578	566 SerLeuAspHisValGlnArgArg	Ş
GGCCATTTCCATGGCCGCGGCCACCTCCACAGCTCTA 2310	2251 TTTGGGGAGCTGCAGACTGTCTCGGCCATT	В
SerLeuSerAlaSerSerGlyTrpAsnGluSerCysSerSerGlnSerAspIle 565	548SerLeuSerAlaSerSerGlyTrp/	δ
TTTAAGAGGATAGAACCCATTACACATGAGCAGGCTTTAGATGTCAGTGAGCAAGGGCCT 2250	2191 TTTAAGAGGATAGAACCCATTACACATGAGG	B
547	ğ	Ş
CTCCAAGTTCTGGAAACGTTTACAGTATGAAATGCCT 2190	2131 GGACCAAAATGCAACAAGTTGAACTCCAAGT	멍
GlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuPro 545	526 GlyGluLysSerLysHisSerGlySerLysI	Ş
TACCAGGAGGTGGAGGCCCTGAAGCACCATCAAGCTCCTGACGGTCATTAAATGGCAT 2130	2071 TACCAGGAGGTGGAGGCCCTGAAGCACACCA	망
SerValSerPheValSerTrpLys 525	515 LeuLysGlu	δ
ATTAAAGTGATTCTAATTGAATGCAGTGAACTGAGAGGAATTATGAAC 2070	2023 ATTAAAGTGATTCTAATTGAATGCAGTGAA	рb
rArgProLeuGluHisProHisProGlyIleLeuGln 514	496LysLeuIleValValGluTyrArgProl	Ş
GGAAACCAGACTTCGAAATATGCTTGTGACTGGAGAA 2022	1969 TGGAGCATCTTTGAGCTGGAAACC	B
IleSerMetLeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThr 495	478 IleSerMetLeuGluPheLysLeuGlyVall	Ş
GTAGATCAAAGCAAGCGGCTGATTATTGTCATGACCCCAAATTACGTAGTTAGAAGGGGC 1968	1909 GTAGATCAAAGCAAGCGGCTGATTATTGTC	망
eValValLeuSerProAspTyrValThrGluLysSer 477	458 IleGlnArgSerArgArgMetIleValValI	Ś
TTTATACCAGATAGAGATTTAATCCCAACTGGAACATACAT	1849 TTTATACCAGATAGAGATTTAATCCCAACTO	Db
uProGlyGlyAsnThrValGluAlaValPheAspPhe 457	438 CysllePheAspArgAspSerLeuProGly	Ş
ACCTGATATGCTTGAAAAGCATTATGGATATAAGTTG 1848	1789 GAACGTTTTGCCCTTGAAATCCTACCTGAT	В
GluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeu 437	418 GluGluPheValLeuLeuThrLeuArgGly	Ś
GCATACTTATCATACACCAAAGTGGATCCTGACCAGTGGAATCAAGAGACTGGGGAAGAA 1788	1729 GCATACTTATCATACACCAAAGTGGATCCTO	рь
AsnAlaGluGlu 417	407 IleTyrValSerTyrAlaArg	Ş
	1669 CTCTTCTACAGGAATCATTTTGGAGCTGAA	망
YThraspGluThrIleLeuaspGlyLysGluTyrasp 406	387 LeuPheTyrArgAlaHisPheGlyThrAspO	Ş
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Query Match:
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17-NOV-1997;
12-MAR-1998;
18-MAR-1998;
15-APR-1998;
                                                                Local Similarity:
                                                                                                                                      mammalian physiology such as morphogenesis of immune system function. The invention particularly relates to nucleic acids, proteins and antibodies which regulate development and/or the immune system. The invention also relates to antibody fragments which specifically bind to antigenic fragments of a primate interleukin (IL)-1 receptor like molecules such as IL-1 receptor DNAX designation (IL-IRD). The antibody fragments of the invention are useful to treat conditions exhibiting abnormal expression of the receptors or their ligands which typically will be immunological disorders. The present sequence is a DNA encoding human IL-IRD10 protein.
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                                                                                                                      Sequence 2537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human interleukin-1
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                                                                                                                                                                                                                                                    Disclosure; Column 41-48; 102pp; English.
                                                                                                                                                                                                                                                                             Antibody fragments which specifically bind to primate interleukin 1 receptor-like molecules are useful to treat conditions associated with abnormal expression of the receptor or its ligand, particularly
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97US-065776P.
98US-078008P.
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/product= "Human IL-1RD10 protein"
/note= "CDS does not include start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy;
                                             2.74e-56
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rapy; immunological
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                                                                       Length:
Matches:
Conservative:
                                            Gaps:
                                                       Mismatches: Indels:
                                                                                                                      G; 692
                                                                                                                                                                                                                                                                                                                                               Bazan JF,
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LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp
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CTGCTTGTATGTTTGGTGACCATCTACAAGTGTTACAAGATAGAAATCATGCTCTTCTAC
                                      LeuValValIleLeuIleValValTyrHisValTyrTrpLeuGluMetValLeuPheTyr
                                                                                                                                                                                                                                                              GAAGTTTCCATCTCATTAATT---GTGGACTCTGTGGAAGAAGGTGACTTG---GGAAAT
                                                                                                                                                                                                                                                                                                                                                CGAGTTTGGGAAAGTGACATTAGAATT---
                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCAGTCCTTTAATTTACTGGATGAAAGGAGAAAAATTTATTGAAGATCTGGATGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIle-----
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|||:::||| ::: ||| ::: ||| |||:::
1384 -----TITGAGCTGGAAACCAGACTTCGAAATATGCTTGTGACTGGAGAATTAAAGTG 1437
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                                                                                                                                                                                                                                                                                                                                                                                                     421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 440
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                                     uCysLysProValProGlnGlu-----SerGluThrGlnTrplleGln 655
CTGCCGCTG-TTGCCAAGGGAGACCAGTATATCCAGTGTGATATGGTGACAG
                                                                                         CCACAGACAAAATCGAGCAGGAGCAGAATCCAGATGAGGCCCACACAAACAGTGCCATC 1959
                                                                                                                                                                                 TCCATAGGCAATCAGCATACCTACTGTAACATCCCTATGACACTCATCAACGGGCAGCGG 1899
                                                                                                                                                                                                                                                                                                                     GluLeuGlnSerSerGluArgAlaAlaGlySerProProAlaProGly***MetSerLys 601
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Search completed: April 30, 2003, 10:53:14
Job time : 318 secs

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Command line parameters:

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-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US10061727 @CGN 1 1 32 @runat _23042003 083117 _7926 -NCPU=6 -ICPU=3
-NO XLDXY -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WAEN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
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Maximum
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Match Length DB
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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US-08-991-944-1
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US-09-173-151A-3
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US-09-173-151A-3
US-09-173-151A-34
US-08-996-338-7
US-08-604-333-1
US-09-110-618-1
US-09-578-178-1
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US-09-578-178-1
US-09-173-151A-9
US-07-821-716-3
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e e e 122	25,1,1,1	e e 1, 7, 3, e e 1, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7,	Sequence 2, Sequence 38, Sequence 4, Sequence 1, Sequence 3, Sequence 15,	<u>, , , , , , , , , , , , , , , , , , , </u>
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## ALIGNMENTS

US-08-991-944-1

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Sequence 1, Application US/08991944
Patent No. 6280955
GENERAL INFORMATION:
                                TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Zha
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                        TELEPHONE:
                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                   ENGTH:
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T: 75 DENISE DRIVE
HILLSBOROUGH
nucleic acid
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                 1740 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 10..1719
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                                                                                                                                                                                                                                                                                                                    PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp
                                                                                                                                                                                             ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly 180
                                                                                                                                                                                                                                      ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
                                                                                                                                                                                                                                                                            TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer
                                                                                                                                                                                                                                                                                                                                                                      GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
                                    CysTyrLys11eGlnAsnPheAsnAsnVall1eProGluGlyMetAsnLeuSerPheLeu 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGAT 129
GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTTCTGATGGATTCTCGCAATGAGGTT
          GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal
                                                                            CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA
                                                                                     ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla
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281 TrpTrpTht11elaspGlykystysProAspAsp11eThr11eAspValThr11elaspGl) 282 TrpTrpTht11elaspGlykystysProAspAsp11eThr11eLaspGlyIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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LOCATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT, APPLICATION DATA:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
AMME: OSMAN, RICHARD
A REGISTRATION UNMBER: 36,627
REFERENCE/DOCKET NUMBER: T97-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4341
TELEPHONE: (650) 343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TENTIL: 1355 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                 141 ProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCys 160
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                                                                                                                                                                                                                                                                                                                                                                                                                       21 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3355 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: HILLSBOROUGH
STATE: CALIFORNIA
                                                              TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSer 140
                                                                                                                                                                                                                                                                 AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
 GCCATGAGATTCCCAGTGCACAAGATGTATATTGAACATGCCATTCATAAGATCACATGT
                                                                                                                                TTCCGGCCCACCCTCCTCAATGACACGGGCAATTACACCTGCATGTTGAGGAACACAACT 494
                                                                                                                                                   PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
                                                                                                                                                                                                  GAGCCCATTAACTTCCGCCTCCCAGAGAATCGCATCAGTAAGGAGAAAGATGTGCTCTGG
                                                                                                                                                                                                                     GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
                                                                                                                                                                                                                                                                                                                                     GAGCCGGCTCGAATCAAGTGCCCCCCTCTTTGAACACTTCCTGAAGTACAACTACAGCACT
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Matches:
Conservative:
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Indels:
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516 1679	497 LeuIleValValGluTyrArgProLeuGluHisProHisProGlyIleLeuGlnLeuLys	음 성
496 1625	481 LeuGluPheLysLeuGlyValMetCysGlnAsnSerIleAlaThrLys	B 정
480 1574	461 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet	망 왕
460 1514	441 AspārgāspSerLeuProGlyGlyāsnThrValGluālaValPheAspPheIleGlnārg	용 &
440 1454	421 ValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePhe 	B 8
420 1394	401 AspGlyLysGluTyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGluGluBhe 	B 8
400 1334	AlaHisPheGlyThrAspGluThrIleLeu 	B 성
380 1274	361 AlacysGlyPheGlyAlaThrValLeuLeuValValI1eLeuI1eValValTyrHisVal	B 8
360 1214	3GlnLysValProAlaProArgTyrThrValGluLeu              AGAAAGTCATACCACCAAGGTACACAGTAGAACTC	B &
340 1154	321 ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu                 :::   :::	B &
320 1094	9ThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys 	B 8
300 1034	281 TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsmGlu 	B 8
280 974	heLeuMetAspSerArgAsnGluVal   ::          CATTATGGACTCCCACAATGAGGTC	B &
260 914	241 ValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu :::            :::	문 왕
240 854		B &
220 794	nAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 	당 왕
200 734	InAsnPheAsnAsnVallleProGluGlyMetAsnLeuSerPheLeu 	문왕
180 674	161 ProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly	B 8

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Patent No. 6326472
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER-DOS/MS-DOS
COPPRATING SYSTEM: PC-DOS/MS-DOS
COPPRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
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                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 15-OCT-1997
                                                                                                                                                                                                                                            FILING DATE: 15-APR-1998 PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 60/065,776
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REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
FELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
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                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 6 FILING DATE: 17-NOV-1997
                                                      NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                             FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                           APPLICATION NUMBER:
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Debets, Johannes Eduard
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Best Local Similarity:
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                                                    CTTAAATAT-----GAAGGAAAACTT-----GTAAGACGAACAACTGAATTGAAAGTT
                                                                                     ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal
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41 ArgLeuAlaLeu		~~
521 PheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeu 	μ	ु र
510 ProGly	بر	ĕ ₹
493 IleAlaThrLysLeuIleValValGluTyrArgProLeuGluHisProHis:	٠.	ট ই
473 ValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGlnAsnSer:::       :::	٠,	ु र
453 AlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTyr 472 ::::::::::::::        :::   :::     ::	н.	£ .
433 PheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGlu 452 :::	н.	ु स्
414AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 4	н.	ē ₹
402 GlyLysGluTyrAspIleTyrValSerTyrAlaArg	н .	ਰ ਵ
382 TrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAsp 401	<u>,,</u>	ਲੇ ਵ
362 CysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyr 381	<u></u>	₽ ×
342 AlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeuAla 	<u>.</u>	₽ ₹
322 ThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluVal 3		Ö
313ThrGlnIleLeuSerIleLysLysVal 3		9 3
293 ThrileAspValThrileAsnGluSerIleSerHisSerArgThrGluAspGluThrArg 312                 859TTTATTGAAGAACTGGCAGGTCACATTAGAGAAGGTGAAATAAGG 903		₽ ₹
273 LeuMetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIle 292 :::    :::    :::    :::    :::    :::		के द
253 ValTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPhe 272		ਰ ₹
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APPLICANT: Timans
APPLICANT: Debets
                                                                   PILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION UNWBER: US 60/
PILING DATE: 18-MAR-1998
PRIOR APPLICATION UNWBER: US 60/
APPLICATION NUMBER: US 60/
PILING DATE: 15-OCT-1997
ATTORNEY/AGENT INPORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 60/065,776
APPLICATION APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION NUMBER: US 60/095,987
APPLICATION NUMBER: US 60/095,987
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/081,883
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TELECOMMUNICATION INFORMATION:
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              NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0: FILING DATE: 14-OCT-1998
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Palo Alto
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Debets, Johannes Eduard Maria
Antonius
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                                                                                                                    US 60/062,066
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Best Local Similarity:
Query Match:
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; LOCATION: 1350..1351;
; OTHER INFORMATION: /note=
US-09-173-151A-1
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NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME/KEY:
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MOLECULE TYPE:
HYPOTHETICAL:
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OTHER INFORMATION: /note=
FEATURE:
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NAME/KEY:
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LOCATION:
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LOCATION: 1033..1034
OTHER INFORMATION: /note=
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                                                                    SerThrAlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAsp
                                                                                              GCAGGTGAACCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTAT
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLys 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTGACAATCCTGAAGAAGAGCAGTTTGCTCTTGAAGTACTGCCAGATGTCCTGGAAAAA 1296
                                               -----AsnAlaGluGluGluBheValLeuLeuThrLeuArgGlyValLeuGluAsn 431
                                                                                                                AspGlyLysGluTyrAspIleTyrValSerTyrAlaArg-----
                                                                                                                                                                                  TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu 400
                                                                                                                                                                                                                                                                                                                                                             GTTGTGGAAGCTGACCTG---GCGAATTATACCTGCCATGTTGAAAACCGAAATGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------TTATTGAAGAACTGGCAGGTCACATTAGA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleThrIleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThr 311
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US-09-173-151A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1471
                                                                                                                                                                                                                                     PRILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
PRIOR TOATION NUMBER: US 60/078,008
                                                                            APPLICATION NUMBER: FILING DATE: 10-AUG-PRIOR APPLICATION DATA:
                                                                                                                                                          FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 15-APR-1998
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 60/065,776
                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, VOURTENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IIILE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                    APPLICATION NUMBER: FILING DATE: 18-MAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACTATATTCTCAGACGGGGATGGAGTATT-----TTCGAACTGGAAAGCAGACTCCAT 1470
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Palo Alto
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Kastelein, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sana, Theodore R.
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                                                                                               UMBER: US 60/095,987
10-AUG-1998
                                        18-MAR-1998
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                                                         US 60/078,416
                                                                                                                                                                                  US 60/081,883
US 60/062,066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-173-151A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-OCT-1997
ATTORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 CysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluProAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              LysValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsnSerPro 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCTTT-----GACGGAAGTAGAATGAGCAAAGAAGAAGACTCCATTTGGTTCCGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSer 63
  --- GGAGGCTTTGTTGTGAGAAGAACTACTGAATTAACTGTTACA---
                                    GluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237
                                                                                                     SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrPro
                                                                                                                                                               TACAAGGAATGCAGGACAAAAACATGGAGGCCAAGTATTGTATTCAAAAGAGATACTCTG
                                                                                                                                                                                                                                             ATTTCATGCCGTGACATAGAGGATTTTCTACTGCCAACCAGAGAACCTGAAATCCTTTGG
                                                                                                                                                                                                                                                                                                                                                                    MetLysLeuProValHisLysLeuTyrIleGluTyrGly------IleGlnArg
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                                                                              CTTATAAGAGAAGTCAGAGAAGATGACATTGGAAATTATACCTGTGAATTAAAATAT---
                                                                                                                                                                                                   TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu 197
                                                                                                                                                                                                                                                                                   IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177
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AGTGAGCAAGGGCCTTTTGGGGAG 1665	O ATAGAACCCATTACACATGAGCAGGCTTTAGATGTCAGTGAGCAAGGGCCTTTTGGGGAG	160	뮍
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CAGTATGAAATGCCTTTTAAGAGG 1605		154	90
ArgLeuAlaLeuProLeuArg 547	9	52	ð
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14		1438	망
ProGlyIleLeuGlnLeuLysGlu 517		498	ફ
:::     CTTGTGACTGGAGAAATTAAAGTG 1437		1384	Дb
IleAlaThr		481	Ś
ValThrGluLysSerIleSerMet 480     :::  TAGTTAGAAGGGGCTGGAGCATC 1383	1 SerArgArgMetIleValValLeuSerProAspTyrValThrGluLysSerIleSerMet	461 1324	£.
HIII EATGTGGCAAGATGTGTAGATCAA 1323		126	<b>D</b>
AlaValPheAspPheIleGlnArg 460		441	Ş
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		421	₹
AsnAlaGluGluGluPhe 420          3AGACTGGGGAAGAAGAACGTTTT 1203	0 SerTyrAlaArg	410 1144	당. 원
AATAAAGATTATGATGCATACTTA 1143		1084	뮍
3lyLysGluTyrAspIleTyrVal 409		390	S
<pre>TrpLeuGluMetValLeuPheTyr 389 :::   :::::             NAGATAGAAATCATGCTCTTCTAC 1083</pre>	O LeuValVall1eLeuI1eValVylHisValTyrTrpLeuGluMetValLeuPheTyr	370 1024	B 8
GAGGCCTTGGTGCTATACTCTTG 1023	4	964	DЬ
ysGlyPheGlyAlaThrValLeu 369	O LysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrValLeu.	350	Ş
AlaLysAlaAlaLysValLysGln 349 .:: CGACACGCCAGCGTTCTCCTT 963	O TYTVAICYSHISAlaArgSerAlaLySGlyGluValAlaLySAlaAlaLySValLySGln	33( 91(	B
HAAGAAGGTGACTTGGGAAAT 909		856	Дb
ChrSerGluAspLeuLysArgSer 329	0	310	ঠ
-:: -CTTAAGGAGCATCTTGGGGAACAG 855	CGAGTTTG	805	DЪ
[leSerHisSerArgThrGluAsp 309	ThrileAspValThrileAs	293	Ş
		745	DЬ
ysProAspAspIle 292	•	276	ફ
:::    :::     GCTTTCTTTGGGTACAGCGGAGAT 744		689	DЪ
/alTyrPheSerPheLeuMetAsp 275	Ò	256	Ş
	O HYDRIANIA VALIFICATIVALLI KOLLIKOTI FICHILIBETI I VALIVALLI VALIVALI VAL	N	문 5
λερΗisValValTvrGlu 255	<b>x</b>	23	8

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US-08-996-338-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. book.
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Musashi
APPLICANT: NUENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08996338 Patent No. 6087116
                                                                                                                                            TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-DEC-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JE-MAR-19
FILING DATE: 12-MAR-19
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1960
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: JP 215,488/1997
FILING DATE: 28-UUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patent In ReCURRENT APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1726 CATCCAGATCTCCGTTCTACCTTTCACAACACGTACCATTCACAAATGCGTCAGAAACAC 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1666 CTGCAGACTGTCTCGGCCATTTCCATGGCCGCCGCCGCCACCTCCACAGCTCTAGCCACTGCC 1725
                                                                                                                                                                                                          NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TO)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
TOPOLOGY: linear MOLECULE TYPE: cDN: ORIGINAL SOURCE:
                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602 HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGlu-As 621
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                                                                                                                                               TELEPHONE: ZUE TELEPHONE: ZUE TELEPHONE: ZUE TO TO NO:
                                                           LENGTH: 1620 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20004
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419 Seventh Street, N.W., Suite 300
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SYSTEM: PC-DOS/MS-DOS
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Score: 528.50
Percent Similarity: 46.11%
Rest Local Similarity: 30.05%
Y Match: 14.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 58..1620
; IDENTIFICATION METHOD:
US-08-996-338-7
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234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 HisSerAlaGlyLeuThrLeu---IleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: sig peptide LOCATION: 1..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: lymphoblastoid cell derived from ORGANISM: with Hodgkin's disease INDIVIDUAL ISOLATE: L428 (FERM BP-5777)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 LeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArg
                                                  ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal 233
                                                                                                                                                                                                                                                                                                                                                                                                    CAG------AAATGGAAATTAAATGTCATCAGAAGAAATAAACACAGCTGTTTC 360
                                                                                                                       AAGAAGAACGCCGAGTTT--------GAAGATCAGGGGTATTACTCCTGCGTG
                                                                                                                                                       GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal 213
                                                                                                                                                                                                                            IleThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnVallleProGlu---
                                                                                                                                                                                                                                                                  -----CAGATAACCTGTGAAAAC-----AGTTACTATCAAACACTGGTCAACAGCACA
                                                                                                                                                                                                                                                                                    ACTGANAGACAAGTAACTAGTAAAATTGTGGAAGTTAAAAAATTTTTTT------408
                                                                                                                                                                                                                                                                                                                                                                Asn-----SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154
                                                                                                                                                                                                                                                                                                                                                                                                                                   TyrCysSerLysValAlaPheProLeuGluValValGln-----LysAspSerCysPhe 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTGGCCAGTTGAATGACACAGGATCTTACTTTTTCCAAATGAAAAATTATACT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ph&ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAG---CIGAACCCAAGG---AGTICCICGAGAATIGCITITGCATGATIGIGITITIGGAG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100
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                                                                                                                                                                                            ---TCATTGTATAAGAACTGTAAAAAGCTACTACTGGAGAACAATAAAAACCCCAACGATA 513
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Matches:
Conservative:
Mismatches:
Indels:
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RESU US-0	문 5	5 5	\$ 8	밁	Ş	Db	Ş	Db	Ş	망	Ş	Дb	Ş	망	Ś	DЬ	Ş	Db	Ş	В	Ş	Вb	Ş	Вb	8.	Ъ	Ś	рb	Ś	Db	ş	ф
RESULT 7 US-08-604-333-1 ; Sequence 1, Application US/08604333	16 TCTTATAACTCAAGGTTCTGGAAGAACCTTCTTTACTTAATGCCTGCAAAAACAGTC 1	549	5 1	1402 ATTAAAATAATCTTAATTGAATTTACACCTGTTACTGACTTCACATTCTTGCCC 1455	493 IleAlaThrLysLeuIleValValGluTyrArgProLeuGluHisProHisPro 510	1342 TCTAATGAGGTCAGGTATGAACTTGAAAGTGGACTCCATGAAGCATTGGTGGAAAGAAA	474 ThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGlnAsnSer 492	1282 ATCCACTCACTGATAGAGAAAAGCCGAAGACTAATCATTGTCCTAAGTAAAAGTTATATG 1341	454 ValPheAspPhelleGlnArgSerArgMetlleValValLeuSerProAspTyrVal 473	1222 GGGTATAAGTTATGCATATTTGAAAGGGATGTAGTGCCTGGAGGAGCTGTTGTTGATGAA 1281	434 GlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThrValGluAla 453	1162 AATGGAGAGGACCACCTTTGCTGTGGAGATTTTGCCCCAGGGTGTTGGAGAAACATTTT 1221	414 AsnAlaGluGluGluGheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPhe 433	1102 TTAACAGATGGAAAAACATATGATGCTTTTGTGTCTTACCTAAAAGAATGCCGACCTGAA 1161	399 IleLeuAspGlyLysGluTyrAspIleTyrValSerTyrAlaArg 413	1042 GTCATTTATAGAGTTGACTTGGTTCTATTTATAGACATTTAACGAGAAGAGATGAAACA 1101	379 HisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThr 398	982 AGAGGAATGATAGCTGTTTGATCTTGGTGGCAGTAGTGTGCCTAGTGACTGTGTGT 1041	362 CysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyr 378	934 ATCTTGGTGAGAAAAGACATGGCTGATATCCCAGGGCCACGTCTTCACA 981	346 LysValLysGlnLysValProAlaProArgTyrThrValGluLeuAla 361	874 CTAAATGTTTTATATAATTGCACTGTGGCCAGCAGGCACGGGAGCCACAGACACCAAAAGCTTC 933	326 LeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAla 345	814 CCAGAAGGCAAATGGCATGCTTCAAAAGTATTGAGAAATAATAGTGAAAAGCAAT 873	314GlnIleLeuSerIleLysLysValThrSerGluAsp 325	781 ATACATGAAGAGAAAAGAATGAGAATTATGACT 813	294 IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr 313	721 CTGAATGAAGAGGATGTAATTTATTGGATGTTCGGGGAAGAAAATGGATCGGATCCTAAT 780	274 MetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThr 293	679 GTGGAATTAGGAAAAAACGTAAGGCTCAACTGCTCTGCTTTG 720	254 TyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeu 273	619 GTGGAAGATCGCAGTAATATAGTTCCCGGTTCTTCTTGGACCAAAGCTTAACCATGTTGCA 678

; Sequence 1, Application US/08604333; Patent No. 5776731; GENERAL INFORMATION: APPLICANT: Parnet, Patricia et al.; APPLICANT: Parnet, Patricia et al.; TITLE OF INVENTION: Receptor Designated

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                                                                                                                                                                                                                                                                                                                         ent Similarity:
Lost Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                        US-10-061-727-2 (1-687) x US-08-604-333-1 (1-1626)
                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
US-08-604-333-1
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1626 base pairs TYPE: nucleic acid TYPE: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/604,333
FILING DATE: 21-FEB-196
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKST NUMBER: 2619
TELEPOMUNICATION: 1206) 587-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: sing
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
INMEDIATE SOURCE:
CLONE: hu2F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: mat peptide
LOCATION: 58.1623
FEATURE:
NAME/KEY: sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
139 CATGAGATTGAAACAACCAACCAAAAGCTGGTACAAAAGCAGTGGATCACAGGAACATGTG 198
                                                                106 TTCTATCTGAAACATTGC------138
                            62 HisSerAlaGlyLeuThrLeu---IleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
                                                                                                                                                                                                    43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
                                                                                                                                     64 TGT----
                                                                                                                                                                   24 CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
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LOCATION:
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51 University Street
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1..1626
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528.00
46.03%
30.00%
14.39%
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Matches:
Conservative:
Mismatches:
Indels:
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174
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215
98
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432	AsnAlaGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu	414	S
1161	ACATTAACAGATGGAAAAACATATGATGTTTTTGTGTCTTAACTAAAAGAATGCCGACCT	1102	ᅡ
413	ThrileLeuAspGlyLysGluTyrAspIleTyrValSerTyrAlaArg	398	Ş
397	TyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu:::	378 1042	B &
1041		985	рь
377	AlaCysGlyPheGlyAlaThrValLeuLeuValValIteLeuIleValVal	361	Ş
984	ATCTTGGTGAGAAAAGCAGACATGGCTGATATCCCAGGCCACGTCTTCACA	934	문
360	LysValLysGlnLysValProAlaProArgTyrThrValGluLeu	346	Ş
933		874	Db
345	LeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAla	326	γQ
873	CCAGAAGGCAAATGGCATGCTTCAAAAGTATTGAGAATTGAAAATATTGGTGAAAGCAAT	814	ДD
325	GlnIleLeuSerIleLysLysValThrSerGluAsp	314	Ş
813	ATACATGAAGAAAAGAAATGAGAATTATGACT	781	Db
313	IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr	294	γQ
780	CTGAATGAAGAGGATGTAATTTATTGGATGTTTÇGGGAAGAAAATGGATCGGATC	721	ф
293	MetAspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThr	274	Q
720	GTGGAATTATCTGCTTTG	679	ДĎ
273	TyrGluLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeu	254	Ą
678	GTGGAAGATCGCAGTAATATAGTTCCGGTTCTTCTTGGACCAAAGCTTAACCATGTTGCA	619	Дb
253	ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal	234	Ş
618	CATTTCCTTCATCATAATGGAAAACTATTTAATATCACCAAAAACCTTCAATATAACAATA	559	ДĎ
233	ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal	214	Qy
558	AAGAAGAACGCCGAGTTTGAAGATCAGGGGTATTACTCCTGCGTG	514	ДĎ
213	GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal	194	Ş
513	TCATTGTATAAGAACTGTAAAAAGCTACTACTGGAGAACAATAAAAACCCAACGATA	457	ДЪ
193	IleThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGlu	175	Ş
456	CAGATAACCTGTGAAAACAGTTACTATCAAACACTGGTCAACAGCACA	409	Db
174	<pre>IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr</pre>	155	Ş
408	Ç.	361	DЪ
154	AsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly	139	Ş
360	CAGAAATGGAAATTAAATGTCATCAGAAGAAATAAACACAGCTGTTTC	313	DЪ
138	TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPhe	121	Ś
312	TTTTGGCCAGTTGAGTTGAACACAGGATCTTACTTTTTCCAAATGAAAAATTATACT	253	ДĎ
120	PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr	101	₽.
252		199	당
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Patent No. 6090918
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et (
                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/01
PILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn
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                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1516 CTTTCTTATAACTCAAGGTTCTGGAAGAACCTTCTTTACTTAATGCCTGCAAAAACAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1282 GAAATCCACTCACTGATAGAGAAAAGCCGAAGACTAATCATTGTCCTAAGTAAAAGTTAT 1341
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                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1342 ATGTCTAATGAGGTCAGGTATGAACTTGAAAGTGGACTCCATGAAGCATTGGTGGAAAGA 1401
                                ANTI-SENSE:
                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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CLONE: hu2F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
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                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 2619
                                                                                                                                                                                                                                                             NAME: Anderson, Kathryn A. REGISTRATION NUMBER: 32,17
                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                             LENGTH:
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                                                                                                           nucleic acid
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Microsoft Word, Version 5.1a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                              (206) 233-0644
                                                                              linear
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Percent Similarity:
Best Local Similarity:
Query Match:
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NAME/KEY:
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619 GTGGAAGATCGCAGTAATATAGTTCCGGTTCTTCTTGGACCAAAGCTTAACCATGTTGCA 678
                                                                                                                            514 AAGAAGAACGCCGAGTTT---
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                             234 ValGlySerProLysAsnAlaValProProValIleHisSerProAsnAspHisValVal
                                                                                                                                                                                               457 ---TCATTGTÄTAAGAACTGTAAAÄÄGCTACTACTGGAGÄACÄÄTAAAAACCCAACGATA
                                                                                                                                                                                                                                                                                           155 IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr
                                                                                                                                                                                                                                                                                                                             361 ACTGAPAGACAAGTAACTAGTAAAATTGTGGAAGTTAAAAAATTTTTT-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla
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                                                                                                                                                           GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal
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                                                             CATTICCTTCATCATAATGGAAAACTATTTAATATCACCAAAACCTTCAATATAACAATA
                                                                                            ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal
                                                                                                                                                                                                                                                                                                                                                                                            CAG-----AAATGGAAATTAAATGTCATCAGAAGAAATAAACACAGCTGTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTGGCCAGTTGAGTTGAATGACACAGGATCTTACTTTTTCCAAATGAAAAATTATACT
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ADDRESSEE: Kathryn A. Anderson,

Immunex Corporation

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US-09-578-178-1
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                    Sequence 1, Application US/09578178
Patent No. 6451760
GENERAL INFORMATION:
APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated
NUMBER OF SEQUENCES: 5
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CORRESPONDENCE ADDRESS:
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US-10-061-727-2 (1-687) x US-09-578-178-1 (1-1626)
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                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
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INFORMATION FOR SEQ ID NO:
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NAME/KEY:
LOCATION:
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NAME/KEY:
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REFERENCE/DOCKET NUMBER: 26:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Ploppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of COMPUTER: Apple Maci
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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 139
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Anderson, Kathryn REGISTRATION NUMBER: 32,
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                                                           TTCTATCTGAAACATTGC----
                            HisSerAlaGlyLeuThrLeu---IleTrpTyrTrpThrArgGlnAspArgAspLeuGlu 80
                                                                                         AlaArgIleLys---CysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
                                                                                                                                                      CysAspAspTrpGlyLeuAspThrMetArg---GlnIleGlnValPheGluAspGluPro 42
CATGAGATTGAAACAACCACCAAAAAGCTGGTACAAAAGCAGTGGATCACAGGAACATGTG
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Matches:
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Indels:
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ACATTAACAGATGGAAAAACATATGATGCTTTTGTGTCTTACCTAAAAGAATGCCGACCT 1161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TCATTGTATAAGAACTGTAAAAAGCTACTACTGGAGAACAATAAAAACCCAACGATA 513
                           TGTGTCATTTATAGAGTTGACTTGGTTCTATTTATAGACATTTAACGAGAAGAGATGAA
                                                                                                                           TyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu 397
                                                                                                                                                                                                                    AlaCysGlyPheGlyAlaThrValLeuLeu-----ValValIleLeuIleValVal 377
                                                                                                                                                                                                                                                                                                                                                      CTAAATGTTTTATATAATTGCACTGTGGCCAGCACGGGAGGCACAGACACCAAAAAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                            LeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAla 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATA------CATGAAGAGAAATGAGAATTATGACT
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                                                                                                                                                                             --- AGAGGAATGATCATAGCTGTTTTGATCTTGGTGGCAGTAGTGTGCCTAGTGACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- AAATGGAAATTAAATGTCATCAGAAGAAATAAACACAGCTGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GlnIleLeuSerIleLysLysValThrSerGluAsp 325
                                                                                                                                                                                                                                                                                                        ---- valproAlaProArgTyrThrValGluLeu 360
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               TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1563 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                       APPLICATION NUMBER: JP 291,837/1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 2:
FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                                                                    FILING DATE: 12-MAR-PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                    NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlavalPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerProAspTyr 472
::: |||::::||||||||||
GAAATCCACTCACTGATAGAGAAAAGCCGAAGACTAATCATTGTCCTAAGTAAAAGTTAT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeu 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHisProHis----- 509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ValThrGluLysSerIleSerMetLeuGluPheLysLeu---GlyValMetCysGlnAsn 491
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1563 base pairs
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OKURA, Takanori
KURIMOTO, Musashi
VENTION: POLYPEPTIDES
                                                                                                                                                                                                                                                                        JP 215,488/1997
                                                                                                                                            25,618
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 TATCAAACACTGGTCAACAGCACA---TCATTGTATAAGAACTGTAAAAAGCTACTACTG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 Gln-----LysAspSerCysPheAsn-----SerProMetLysLeuProVal 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172 GCTTTGCATGATTGTGTTTTGGAGTTTTGGCCAGTTGAGTTGAATGACACAGGATCTTAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AGCAGTGGATCACAGGAACATGTGGAG---CTGAACCCAAGG---AGTTCCTCGAGAATT 171
                                                                                                                                                                                                                                                                                                                                        478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             340 AAAAAATTTTTT-----AGTTAC 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 TTTTTCCAAATGAAAATTATACTCAG------AAATGGAAATTAAATGTCATC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ThrCysMetLeuArgAsnThrThrTyrCysSerLysValAlaPheProLeuGluValVal 132
                                                                                                                                                                                                 246 HisSerProAsnAspHisValValTyrGluLysGluProGlyGluGluLeuLeuIlePro 265
                                                                                                                                                                                                                                              538 ACCAAAACCTTCAATATAACAATAGTGGAAGATCGCAGTAATATAGTTCCGGTTCTTCTT
                                                                                                                                                                                                                                                                                      226 ThrArgThrLeuThrValLysValValGlySerProLysAspAlaValProProValIle 245
                                                                                                                                                                                                                                                                                                                                                             206 AsnAsnGlyAsnTyrThiCysValValThrTyrProGluAsnGlyArgThrPheHisLeu 225
                                                                                                                                                                                                                                                                                                                                                                                                                            433 GAGAACAATAAAAACCCAACGATAAAGAAGAACGCCGAGTTT------GAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AGAAGAAATAAACACAGCTGTTTCACTGAAAGACAAGTAACTAGTAAAATTGTGGAAGTT 339
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IDENTIFICATION METHOD:
286 GlyLysLysProAspAspIleThrIleAspValThrIleAsnGluSerIleSerHisSer 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ThrArgGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProGluAsnArgIle 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleGlnValPheGluAspGluProAlaArgIleLys---CysProLeuPheGluHisPhe 53
                                                                                                                                                                                                                                                                                                                                        GATCAGGGGTATTACTCCTGCGTGCATTTCCTTCATCATAATGGAAAACTATTTAATATC 537
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                                                          TGC-----TCTGCTTTGCTGAATGAAGAGGATGTAATTTATTGGATGTTCGGG 699
                                                                                                                                                         GGACCAAAGCTTAACCATGTTGCAGTGGAATTA-----GGAAAAAAACGTAAGGCTCAAC
                                                                                                       CysThrValTyrPheSerPheLeuMetAspSerArgAsnGluValTrpTrpThrIleAsp 285
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	; TITLE		; APPLICANT:				; Pacent No.	; Sequence	RESULT 11 US-09-173-151A-9	DD 1495	Qy 543 I	Db 1435 <i>I</i>	Qy 523 S	Db 1375 (	Qy 505 I	Db 1321 C	Оу 486 -	Db , 1261 A	Qy 466 V	Db 1201 C	Qy 446 P	Db 1141 C	Qy 426 A	Db 1081 T	Qy 411 T	1021	Оу 391 А	961	Qy 371 V	913	Qy 354 P	Db 853 G	Qy 338 L	Db 793 A		Db 733 G	Оу 306 А	рь 700 G	
CORRESPONDENCE ADDRESS: ADDRESSEE: DNAX Research Institute	OF INVENTION: Human Receptor Froteins; Related Reagents and methods	Kastelein, Robert A.	Bazan, J. Ferna	CANT: Antonius	: Debets, Johannes Ed	E 3	~	9, Application US/09173151A	151A-9	TIARIUCCIUCARARACAUIC 1515	AlaLeuProLeuArgSerLeu 549	TAAATCTCTTTCTTATAACTCAAG	SerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeu 542	GTTACTGACTTCACATTCTTGCCCCAATCACTAAAGCTTTTGAAATCTCACAGAGTTCTG 1434	522	CATGAAGCATTGGTGGAAAAAATTAAAATAATCTTAATTGAATTTACACCT 1374	tCysGlnAsnSerIleAlaThr 	TTGTCCTAAGTAAAAGTTATATGTC		CCTGGAGGAGCTGTTGTTGATGAAATCCACTCACTGATAGAGAAAAAGCCGAAGACTAATC 1260	roGlyGlyAsnThrvalGluAlaValPheAspPheIleGlnArgSerArgArgMetIle 465	CCCAGGGTGTTGGAAAACATTTTGGGTATAAGTTATGCATATTTGAAAGGGATGTAGTG 1200	ArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeu 445	CCTAAAAGAATGCCGACCTGAAAAT	TyrAlaArgAsnAlaGluGluGluGluDheValLeuLeuThrLeu 425	CATTTAACGAGAAGAGATGAAACATTAACAGATGGAAAAACATATGATGCTTTTGTGTCT 1080	ThrIleLeuAspGlyLysGluTyrAspIleTyrVal	:::     ::::      :::::::	ValValIleLeuIleValValTyrHisValTyrTrpLeuGluMetValLeuPheTyrArg 390	CACGTCTTCACAAGAGGAATGATCATAGCTGTTTTGATCTTGGTGGCA 960	roArgTyrThrValGluLeuAlaCysGl\PheGlyAlaThrValLeuL	GAGGCACAGACACCAAAAGCTTCATCTTGGTGAGAAAAGACATGGCTGATATCCCAGGC 912	lLysGlnLysVa	::: :::	leLysLysValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAla 337	 	lnIl	GAAGAAAATGGATCGGATCCTAATATA	

ADDRESSEE: DNAX Research Institute

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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
; LOCATION:
US-09-173-151A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/078,008
FILING DATE: 12-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 60/095,987
APPLICATION UNMBER: US 60/095,987
FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (650)852-9196
TELEPAX: (650)496-1200
INFORMATION FOR EGO ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DAILS.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
14.090
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/065,776

APPLICATION NUMBER: 17-NOV-1997

APPLICATION NUMBER: 17-NOV-1997
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                   247 GATTTACCAGAGCCACAGAAATCACATTTCTGCCACAGAAATCGACTCTCACCAAAACAA 306
                                                                          187 ACAAAAAAACTCCTTTGGACATATTCTACAAGGAGTGAAGAGGGAATTTGTCTTATTTTGT 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
CITY: P
STATE:
                                                                                                                                                                                 11 TyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArgCysAspAspTrpGlyLeuAsp 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2314 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/173,151A FILING DATE: 14-OCT-1998
                                    48 ProLeuPheGlu-----
                                                                                                            31 ThrMetArgGlnIleGlnValPhe-----GluAspGluProAlaArgIleLysCys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   f: 901 California Avenue
Palo Alto
California
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44.25%
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                                -----HisPhe------
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Matches:
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398 ThrileLeuAspGlyLysGluTyrAspIleTyrValSerTyrAlaArg 413	Ş
1249 CTCTACAGGCACTGGATTGAAATAGTGCTGCTGTACCGGACCTACCAGAGCAAGGATCAG 1308	Db
sValTyrTrpLeuGluMet	Ş
1189 CTGTACATCCTGCTTGGCACCATCGGGACCCTGGTGGCCGTGCTGGCGGGGGAGTGCCCTC 1248	망
euAlaCysGlyPheGlyAlaThrValLeuLeuValVallleL	Ş
1141 AACACAACCCAGTCCGACCGAAAGAAAAGAGAGGAGTGGTGCTC 1188	Db
roAlaPro	Ş
1081 AAAGTCACTCAGGGTGATCTTCGCAGGAAGTTTGTTTGCTTTGTCCAGAACTCCATTGGA 1140	망
320 LysValThrSerGluAspLeuLysArqSerTyrValCysHisAlaArgSerAlaLysGly 339	Ş
A	В
301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319	S
970 AAATGGTACATCAAAGATTCTGACCTAGAGTGGGAAGTCTCAGTACCTGAG 1020	DЬ
281 TxpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu 300	Ş
910 CCTTTAACTATTAGCTGCAAAGCACGATTTGGCTTTGAAAGGGTCTTTAACCCTGTCATA 969	Db
261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal 280	Ş
856 AAACCAGATATTCTGGATCCTGTCGAGGACACACTGGAAGTAGAACTTGGAAAG 909	DЬ
HisVa	Ą
796 AGTTCGTGGACAGTCAGAGCTGTTGTTCAAGTGAGAACCATTGTGGGAGACACTAAACTC 855	Db
221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 240	8
742TATGACTATCACCAGGGCACATATGTATGTGATTACACTCAGTCGGATACTGTG 795	DЪ
201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220	Ş
697 CTCCTCTGTGGAAAGGAGCAACCGAATCGTAGTGGATGAAGTT 741	В
181 CysTyrLysIleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeuSerPheLeu 200	ঠ
640 CTCAGCTGCCAAAGTGATGCACAAAGTCCAGGGGTAACCTGGTACAAGAATGGAAAA 696	DЬ
alAspGlyTyrPhe	Ş
589CATAAGCAAGACCTACTTCTTGGGAGCACTGGCTCTATTTCTTGCCCCCAGT 639	망
144 LeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCysProAsn 162	Ş
	DЬ
124 LysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLys 143	Ş
472 GGGTCATATATTTGTAGACCCAAGATGATTAAGAGCCCCTATGATGTAGCCTGTTGTGTC 531	Db
110 GlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer 123	Ş
415 CACATCATTCAGGACAAATGTACCCTTCACTTTTTGACCCCCAGGGGTGAATAATTCT 471	망
90 AsnArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109	₽.
358 TGGTACCAACCAACCTTCGAATGGAGATCCATTAGAGGACATTAGGAAAAGCTATCCT 414	문
70 TrpTyrTrpThrArgGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProGlu 89	Ş
307 GTCCCTGAGCACCTGCCCTTCATGGGTAGTAACGACCTATCTGATGTCCAA 357	DЬ
54LeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuile 69	Ş

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1993 AGGCTGATAGGAAATTCAAAGAGTCTCCTG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1369 CCAAGTGAGGCCACTTCATCTCTGAGTGAAGAACACTTGGCCCTGAGCCTATTTCCTGAT 1428
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    564 AspIleSerLeuAspHisValGlnArgArgArgSerArgLeuLysGluProProGluLeu 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 LeuProLeuArgSerLeuSerAlaSerSerGlyTrpAsnGluSerCysSerSerGlnSer 563
                                         STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluThrHisLeu 641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGluAsn 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnSerSerGluArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATTTTCAGTGGAAAGGACTCAGTAGAACAGAAACCACTGGGAGGAGCT-CCCAGCCTA 1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGCCTGTGAAAAAC---TCTCAGGGATTCACGTGGAACCAGCTCAGAATTACCTCTAG- 1838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAla 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAGTCTCTACCTCATCTC---GTGAAAAAAAGCTCTCAGGGTTTTGCCCCACAGTTACT 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProLeuGluHisProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSer 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGTGTATGCAGAAGACATTGTGAGCATTATTAAGAGAAGCAGAAGAGGGAATATTTATC 1548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValVal 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValLeuGluAsnGluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGly 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGAGAGGCTTAAAATCAGTTCCTCCCAATTCTAGGTTCTGGGCCCAAAATGCGCTACCAC 1782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGAGCCCCAACTATGTCAATGGACCCAGTATCTTTGAACTACAAGCAGCAGCAGTGAATCTT 1608
                                                                                                                                                                                                                                                                                                                  Application US/07821716
                                                                                                                                                                                      Dower, Steven K.
March, Carl J.
Sims, John
Urdal, David L.
                                                                                51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                  CCAGCACCAAGCAAGCTTGATGGACAATGG
                                                                                                          Immunex Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                    -AATGGG 2058
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores: Pred: No.:
                                                                                                                                                                                                                                                                                                                                                                               Score:
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TELEPAX: (206)
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
1.KNGTH: 2356 base pairs
1.KNGTH: 2356 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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PRIOR APPLICATION NUMBER: US 258756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 125627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Mouse IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRIGINAL SOURCE:
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  387
                                                                                                                                                                285 GAGATTGACGTATGTACAGAATATCCAAATCAGATCGTTTTGTTTTTATCTGTAAATGAA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                  345 ATTGATATTCGCAAGTGTCCTCTTACTCCAAATAAAATGCAC--
                          62 HisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGluGlu 81
                                                                                                                                                                                                     34 GlnIleGlnValPheGluAspGluProAlaArgIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wight, Christopher L. REGISTRATION NUMBER: 31,680 REFERENCE/DOCKET NUMBER: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
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225..1955
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225..281
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282..1952
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                                                                                                                LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
                                                                                                                                                                                                                                                                                                           488.50
43.21%
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Sequence 3, Application Patent No. 5319071
GENERAL INFORMATION: APPLICANT: Dower,

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TÄCGÄTGCCTÄTATTCTTTATCCCAAGACCCTGGGAGÄGGGGTCCTTCTCAGACTTAGAT 1445
                                                                     CTTTGGTACAGGGACTCCTGCTCTGGTTTTCTTTCCTTCAAAAGCTTCAGATGGAAAGACA 1385
                                                                                      LeurheTyrArgAlaHisPheGly-----ThrAspGluThrIleLeuAspGlYLysGlu 404
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                                                                     Sequence 3, Application US/08381603
Patent No. 5858355
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Brans, Christopher H.
APPLICANT: Brans, Christopher H.
APPLICANT: Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer For Treating a Connective Tissue TITLE OF INVENTION: Mammalian Host
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          2039
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                           Philadelphia
              PA
                                        E: Eckert Seamans Cherin & Mellott
1700 Market Street Suite 3232
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FEATURE:
NAME/KEY:
LOCATION:
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 866172
NFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAMB: GOULD, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
TELEPHAX: (215) 575-6015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATION:
COMPUTER: PC COMPATION:
COMPATION SYSTEM: PC COMPATION:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/381,603
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                   208
424 ACACAGGCCACCTTCCCA---CAGCGCTCCACATTGCC---GGGGATGGAAGTCTTGTG 477
                                                                                                                                               304 GTACCTGCCAAGGTGGAGGACTCAGGATATTACTATTGTATAGTAAGAAACTCAACTTAC
                                  140 SerProMetLysLeuProValHisLysLeuTyrTleGluTyrGlyIleGlnArgIleThr 159
                                                                                                        122 CysSerLysValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsn 139
                                                                                                                                                                                102 ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyr 121
                                                                                                                                                                                                                       166 ATTGATATTCGCAAGTGTCCTCTTACTCCAAATAAAATGCAC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GAGATTGACGTATGTACAGAATATCCAAATCAGATCGTTTTGTTTTTATCTGTAAATGAA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                            82 ProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPhe 101
                                                                                                                                                                                                                                                                                                                      62 HisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGluGlu 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 GlnIleGlnValPheGluAspGluProAlaArgIle----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: Mouse T-cell cDNA Library CLONE: Mouse Interleukin-1 Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 1782 base pairs
                                                                         TGCCTCAAAACTAAAGTAACCGTAACTGTGTTAGAGAATGACCCTGGCTTGTGTTACAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
46..1776
                                                                                                                                                                                                                                                                                                                                                                                                  ----LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
                                                                                                                                                                                                                                                                                               -GGCGACACCATAATTTGGTAC-----AAGAATGACAGCAAGACC 246
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484.50
46.04%
25.80%
13.21%
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Matches:
Conservative:
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153
120
225
95
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                                                                                                                                                 363
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491 AsmSerIleAlaThrLysLeuIleValValGluTyrArgProLeuGluHisPro 508	Q
1447 GGCCAGTCATCTGAAGAGCAAATAGCCATATACAATGCTCTCTCATCCAG 1494	•
LeuGluPheLysLeuGlyValMet	Ş
1387 AAGAAAAGCAGGATGATTATCATTCTAGTGAGAGATATGGGAGGCTTCAGCTGGCTG	Db
459 GlnArgSerArgArgMetIleValValLeuSerProAsp	Q
:::	Db .
н	₽
1267 ACTITIGETTTTAAACTGTTGCCTGAGGTCTTGGAGGGGACAGTTTGGATACAAGCTGTTC .1326	ръ
419 GlupheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCys 438	Ş
1207 TACGATGCATATTCTTTATCCCAAGACCCTGGGAGAGGGGTCCTTCTCAGACTTAGAT 1266	Db
405 TyrAspIleTyrValSerTyrAlaArgAsnAlaGluGluGlu 418	Ş
1147 CTTTGGTACAGGGACTCCTGCTCTGGTTTTCTTCCTTCAAAAGCTTCAGATGGAAAGACA 1206	οь
387 LeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGlu 404	৪
1087 CTCACGGCTACAATTGTATGCTGTGTGTGTGCATCTATAAAGTCTTCAAGGTTGACATAGTG 1146	рb
367 ThrValLeuLeuValValIleLeuIleValValTyrHisValTyrTrpLeuGluMetVal 386	Ş
1027 GTGCAGTTAATATACCCAGTCCCTGACTTCAAGAATTACCTCATCGGGGGCTTTATCATC 1086	Дb
347 ValLysGlnLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAla 366	Ş
973 CGCTATCCGTTTATCTGTGTTGTTAAGAACACAAATATTTTTGAGTCGGCGCAT 1026	Db
327 LysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLys 346	Ş
913 AAAAGAAAATACACACTCATTACAACACTTAACATTTCAGAAGTTAAAAAGCCAGTTTTAT 972	рb
308 GluAspGluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu 326	Ş
853 ATTGAATGGAATGATCCATTTCTAGCTGAAGACTATCAATTTGTGGAACATCCTTCAACC 912	рb
296 ValThrIleAsnGluSer	Ş
817TCAGACCTTGTCTACTGGAAGTGGAATGGATCAGAA 852	Ъ
276 SerArgAsnGluValTrpThrIleAspGlyLysLysProAspAspIleThrIleAsp 295	Qy
766 GCTGACCCAGGATCAATGATACAACTGATCTGCAACGTCACGGGCCAGTTC 816	рь
256 LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275	Q
712 GAAAACAAGAGGGACAGACCTGTTATCCTGAGCCCTCGGAATGAGACGATCGAA 765	DЪ
236 SerProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGlu 255	Ş
652 TATACGTTCCGGGGAAGCAATATCCGGTCACACGAGTAATACAATTTATCACAATAGAT 711	рь
216 TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGly 235	Q
592 AAACTGTTGGTGAGGAATGTGGCTGAAGAGCACAGAGGGGACTATATATGCCGTATGTCC 651	B
198 SerPheLeulleAlaLeulleSerAsnAsnGlyAsnTyrThrCysValValThr 215	Ş
535 TATAAGAACTGTAAACCTCTGCTTCTTGACAACGTGAGCTTCTTCGGAGTAAAAGAT 591	Ъ
178 TyrwetGlyCysTyrLysileGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeu 197	٠ الم
478 TGCCCTTATGTGAGTTATTTTAAAGATGAAATAATGAGTTACCCGAGGTCCAGTGG 534	Db
160 CysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177	Q

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Glorioso, Joseph C.
APPLICANT: Evans, Christopher H.
APPLICANT: Robbins, Paul D.
APPLICANT: Bandara, Geethani
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                            HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE: LIBRARY: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1669
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      TELEPHONE: (215) 575-6000
                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                        MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/924,376 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                         TELEPHONE: (215) 575-6015
                                                                                                                                                                                                                                                                                                    NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 08-MAR-1993
NAME/KEY:
                                           CLONE:
                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Eckert Seamans Cherin & Mellott STREET: 1700 Market Street Suite 3232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
                                                                                                                                            TOPOLOGY:
                                                                                                                                                                      TYPE: • nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleSerLeuAspHisValGlnArgArgArgSerArgLeu 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTCAAGAAAGACCACAGTCTGCAAAGACCAGGTTCTGGAAAAACTTAAGATACCAGATG 1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisProGlyIleLeuGln---LeuLysGluSerValSerPheValSerTrpLysGly---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProLeuArgSerLeuSerAlaSerSerGlyTrpAsnGluSerCysSerSerGlnSerAsp
                                           Y: Mouse T-cell cDNA Library
Mouse Interleukin-1 Receptor
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                                                                                                                                                                                     1782 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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SYSTEM: PC-DOS/MS-DOS
CDS
46..1776
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                                                                                                                           CDNA
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-924-376-3
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308 GluAspGlu---ThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu
                                 853
                                                                                                     817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247
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                                                                                                                                  SerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAsp 295
                                                                                                                                                                                                   LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275
                                                                                                                                                                                                                                       GAAAACAAGAGGGAC---AGACCTGTTATCCTGAGCCCTCGGAATGAGACGATC---GAA
                                                                                                                                                                                                                                                                         SerProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGlu 255
                                                                                                                                                                                                                                                                                                                                         TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGly 235
                                                                                                                                                                                                                                                                                                                                                                                                                                               TATAAGAACTGT---AAACCTCTGCTTCTTGACAACGTGAGCTTCTTCGGAGTAAAAGAT 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCCTTATGTG----AGTTATTTTAAAGATGAAAATAATGAGTTACCCGAGGTCCAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CysProAsnValAspGlyTyrPhe-----ProSerSerValLysProThrIleThrTrp 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACACAGGCCACCTTCCCA---CAGCGGCTCCACATTGCC---GGGGATGGAAGTCTTGTG 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThr 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGCCTCAAAACTAAAGTAACCGTAACTGTGTTAGAGAATGACCCTGGCTTGTGTTACAGC
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                                 ATTGAATGGAATGATCCATTTCTAGCTGAAGACTATCAATTTGTGGAACATCCTTCAACC
                                                                                                                                                                     GCTGACCCAGGATCAATGATACAACTGATCTGCAACGTCACGGGCCAGTTC--
                                                                                                                                                                                                                                                                                                           TATACGTTCCGGGGGAAGCAATATCCGGTCACACGAGTAATACAATTTATCACAATAGAT
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                                                                                                     ---TCAGACCTTGTCTACTGGAAGTGGAATGGATCA----
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                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                   Sequence 3, Application US/08685212
                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Glorio
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                                                      APPLICANT: Glorioso, Joseph C.
APPLICANT: Evans, Christopher H.
APPLICANT: Robbins, Paul D.
APPLICANT: Bandara, Geethani
TITLE OF INVENTION: Gene Transfer For Treating a
TITLE OF INVENTION: Connective Tissue of a Mammalian Host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1447
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                    NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                 US-10-061-727-2 (1-687) x US-08-685-212-3 (1-1782)
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1782 base pairs
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ATTORNEY/AGENT INFORMATION:
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ANTI-SENSE: 1
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APPLICATION NUMBER: US/08/027,750
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ZIP: 19103
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CITY: P
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LOCATION:
                                                                                                                                82
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REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 109070-3
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                                                                                                                                                                                                                                                                  46
                                                                                                                                                                                                                                                                                                                                34 GlnIleGlnValPheGluAspGluProAlaArgIle---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
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CysSerLysValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsn 139
                                                                                                                                                                                              HisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGluGlu 81
                                                              ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyr 121
                                                                                               CCCATATCAGCGGAC---CGGGACTCCAGGATTCATCAGCAGAATGAACATCTTTGGTTT 303
                                                                                                                            ProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPhe 101
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argSerArgArgMetIleValValLeuSerProAsp	459 GlnArgSerArg!
lePheAspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIle 458 	439 IlePheAspArg <i>F</i>     :::      1327 ATTTATGGAAGGG
luPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCys 438        :::	419 GluPheValLeuI        1267 ACTTTTGTTTTF
TyrAspIleTyrValSerTyrAlaArgAsnAlaGluGlu	405 TyrAspileTyrV
LeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGlu 404     ::       	387 LeuPheTyrArgA    :::       1147 CTTTGGTACAGGC
ThrValLeuLeuValVallleLeuIleValValTyrHisValTyrTrpLeuGluMetVal 386 :::    ::: ::::::   CTĈACGGCTACAATTGTATGCTGTGTGCATCTATAAAGTCTTCAAGGTTGACATAGTG 1146	367 ThrValLeuLeuV : 1087 CTČACGGCTACAA
ValLysGlnLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAla 366    :::	347 ValLysGlnLysV    ::: 1027 GTGCAGTTAATAT
rgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAlaLys 346 ::::::    ::::::    ::::::   ATCCGTTTATCTGTGTTGTTAAGAACACAAATATTTTTGAGTCGGCGCAT 1026	327 LysargSerTyrV ::: 973 CGCTATCCGTTTA
GluAspGluThrArgThrGlnIleLeuSerIleLysLysValThrSerGluAspLeu 326 :::        :::    :::       ::: AAAAGAAAATACACACTTACAACACTTAACATTTCAGAAGTTAAAAGCCAGTTTTAT 972	308 GluAspGluT ::: :::   913 AAAAGAAAATACA
ValThrIleAsnGluSerIleSerHisSerArgThr 307 :::    :::     ATTGAATGAATGATCCATTTCTAGCTGAAGACTATCAATTTGTGGAACATCCTTCAACC 912	296 ValThrileAsnG :::    : 853 ATTGAATGGAATG
ArgAsnGluValTrpTrpThrlleAspGlyLysLysProAspAspIleThrlleAsp 295	276 SerArgAsnGluV :::   817TCAGACCTTG
LysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAsp 275	256 LysGluProGlyG :::       766 GCTGACCCAGGAT
YOLYSASNAlaValProProValIleHisSerProAsnAspHisValValTyrGlu 255 	236 SerProLysAsnAla     712 GAAAACAAGAGGGAC
rProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGly 235 	216 TyrProGluAsng           652 TATACGTTCCGG
SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThr 215	198 SerPheLeuIleA    ::: 592 AAACTGTTGGTGA
TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeu 197	178 TyrMetGlyCysT
CysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThrTrp 177	160 CysProAsnValA            478 TGCCCTTATGTG-
SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThr 159 :::	140 SerProMetLysL ::: 424 ACACAGGCCACCT
	364 TGCCTCAAAACTA

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                               545 ProLeuArgSerLeuSerAlaSerSerGlyTrpAsnGluSerCysSerSerGlnSerAsp 564
                       ---CCATTGTCTAAACACCGCTTA 1707
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Search completed: April 30, 2003, 13:03:13 Job time : 93 secs

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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q-/cgn2 /USPTO_spool/US10061727/runat_23042003_083118_8008/app_query.fasta_1.839
-Q-/cgn2 /USPTO_spool/US10061727/runat_23042003_083118_8008/app_query.fasta_1.839
-DB=PublIshed_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER-US10061727 @CGN 1 1 84 @runat_23042003_083118_8008
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 27, Appl
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ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu
                           ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla
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                                                                 TGGTGGACCATTGATGGAAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAA
                                                                           TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu
                                                                                                     GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT
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APPLICANT: Sims, John E.
APPLICANT: Sims, John E.
APPLICANT: Smith, Dirk E.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN
FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR PILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 1077
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NUMBER OF SEQ ID NO Sapiens
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Publication No. US20030049255A1
GENERAL INFORMATION:
NAME/KEY: CDS
LOCATION: (1)..(1077)
OTHER INFORMATION:
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SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLysLys
                              TrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspValThrIleAsnGlu
                                                              GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT
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PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: Patentin version 3.0
SEQ ID NO 27
LENGTH: 2733
TYPE: DNA
ORGANISM: Homo sapiens
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TITLE OF INVENTION: Receptor Based Antagonists,
FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
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Sequence 3, Application US/10011548 Publication No. US20030055218A1 GENERAL INFORMATION:
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             ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
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                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                STREET: 901 California Avenue CITY: Palo Alto CITS: California
                                                                                                                                                                                    COUNTRY: USA
CLASSIFICATION:
                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                 Kastelein, Robert A.
INVENTION: Human Receptor Proteins; Related Reagents
Methods
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 15-OCT-1997 ATTORNEY/AGENT INFORMATION:
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                                 ThrTyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSer-----Cys 137
                                                                                                         TrpPheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThr 119
                                                                                                                                                                                                                                     GGTGAACCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTATAGC
                                                                                                                                                                                          GluGluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGGCCCTTGTGGTCTGTTGTAGTCAGCACAAATCTGAAGATGGTGTCAAAGAGAAAT
                                                                                                                                                              GAAGAGCCCATCATCTTT-----TCAGAGGTCAGGATGAGCAAAGAGGAAGATTCAATA
             TGGTTTCACTCAGCTGAGGCACAAGACAGTGGATTCTACACTTGTGTTTTTAAGGAACTCA
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/081,883 FILING DATE: 15-APR-1998 APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998 APPLICATION NUMBER: US 60/078,416 FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/173,151
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/065,
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (650)496-1200
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Conservative:
Mismatches:
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US-10-011-548-3

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492	173 ValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGlnAsnSer	Qy 4	_
1434	75 GATCTCACAAGATATGTTGAACAAAGCAGAAGACTTATTATCGTGCTAACTCCAGACTAT	13	
472	53	φ	_
1374	<b>~</b> (	<u>.</u>	
452	433 PheGlvTvrLvsLeuCvsIlePheAspArgAspSerLeuProGlvGlvAsnThrValGlu	9 4	_
432 1314	414AshālaGluGluGluGluPheValLeuCeuThrLeuArgGlyValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluBluBluBluPheValLeuGluAshGlu 414AshālaGluGluGluBluBluBluBluBluBluBluBluBluBluBluBluBl	와 12	
1254		<u> </u>	_
413	402 GlyLysGluTyrAspIleTyrValSerTyrAlaArg		_
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401	2 TrpLeuGluMetValLeuPheTyrArqAlaHisPheGlyThrAspGluThrIleLeuAsp		_
381 1134	2 CysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisValTyr	Qy 36 Db 107	
361 1074	342 AlalysalaAlaLysValLysGlnLysValProAlaProArgTyrThrValGluLeuAla	10	_
1017	64	Db 9	_
341	22 ThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluVal	Qy 3	_
963	04 CTTCTCAAAGAGCATCTTGGAGAAAAA	Db 9	_
321		Qy 3	_
903	59TTTATTGAAGAACTGGCAGGTCACATTAGAGAAGGTGAAATAAGG	œ	_
312	93	Qy 2	_
858	814 AGTGGAGAGTCTGGGCCAATGATCTACTGGATGAAAGGAGAAAAG	ръ В	_
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272	ပ္သ	Q 2	_
753	:::        :::	6	_
252	4	Qy 2	_
233 693	114 ValThrTyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysVal :::	Q 2	_
645	96	Db 5	_
213	.94 GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal	27	
585	*:::        ::: 26 GATGTTGTGGTATAAGGAATGCAAGCCAAAAATGTGGAGAGCATAATAATAATACAGAAA	Db 5	_
193	74	Qy 1	_
525	5511eJINATGLIEUTICYSETOASNVALASDAJYTYFTHEKTOSETSETVALLYSEKO 66 ANANGANAGGAGATCTCCTGTCCAGACATGAGATGACTTTANANANGTCCGATCAGGAGCCT	B 5	
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Sequence 1, Application US/10011548 Sequence 1, Application WS/10011548 Publication No. US/20030055218A1 GENERAL INFORMATION: APPLICANT: Timans, Jacqueline C. Bazan, J. Pernando Kastelein, Robert A. TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: ADDRESSE: DNAX Research Institute STREET: 901 California COUNTRY: USA COUNTRY: USA COUNTRY: USA ZIP: 94304-1104 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/10/011,548 FILING DATE: 22-Oct-2001 CLASSIFICATION: <unknown></unknown>	621 AsnHisLeuArgAsnLysSerArgAlaGluIleHis 632	- 601 LysHisArgGlyLysSerSerAlaThrCysArgCysCysValThrTyrCysGluGlyGlu 620	587GluArgAlaAlaGlySerProProAlaProGly***MetSer 600	575 SerArgLeuLysGluProProGluLeuGlnSerSer	555 TrpAsnGluSerCysSerSerGlnSerAspIleSerLeuAspHisValGlnArgArgArg 574	548SerLeuSerAlaSerSerGly 554	541 ArgLeuAlaLeuProLeuArg547 :::   :::::: 1657 GTATATGAAATGCCCATCAAGAAAAAAAAAAATGCTACCTCGGTGCCATGTTCTGGACTCC 1716	21 PheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeu 54 :::	AAACTTCTGTCC 15	493 IleAlaThrLyBLeuIleValValGluTyrArgProLeuGluHisProHis 509 :::	:::    :::

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                            Score:
                                                                                           Pred. No.:
                                                                                                            Alignment Scores:
                                                                                                                                                  US-10-011-548-1
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REGISTRATION NUMBER: 34,090
REPERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEPHONE: (650) 496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 1350..1351
OTHER INFORMATION: /note= "splice junction"
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-WAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1033..1034
OTHER INFORMATION: /note= "splice junction"
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LOCATION: 342..343
OTHER INFORMATION: /not
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LOCATION: 1177..1178
OTHER INFORMATION: '/note= "splice junction"
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LOCATION: 756..757
OTHER INFORMATION: /note= "splice junction"
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LOCATION: 885..886
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LOCATION: 453..454
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TYPE: nucleic acid
STRANDEDNESS: single
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                 Length:
Matches:
Conservative:
Mismatches:
Indels:
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US-10-061-727-2 (1-687) x US-10-011-548-1 (1-1737)

ValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGlyGlu 340 		321 946	B &
AGGCTTCTCAAAGAGCATCTTGGAGAAAAAGAAGTTGAATTGGCACTCATCTTTGACTCA 945	AGGCTTCTCA	986	ф
ThrGlnIleLeuSerIleLysLys 320	Arg	312	φ
TTTATTGAAGAACTGGCAGGTCACATTAGAGAAGGTGAAATA 885	. ;	844	Db
AspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThr 311	IleThrIleA	292	Ş
TTCAGTGGAGAGTCTGGCCCAATGATCTACTGGATGAAAGGAGAAAAG 843	TTCAGTGGAG	796	DЬ
AspSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAsp 291	PheLeuMetA	272	§
AGTGTTATAGATGTCCAGCTGGGTAAGCCTCTGAACATCCCCTGCAAAGCATTCTTCGGA 795	AGTGTTATAG	736	Db
31uLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSer 271		252	ş
GITACAGCITTACICACAGACAAGCCICCCAAGCCATIGITCCCCCAIGGAGAATCAGCCA 735	GTTACAGCTT	676	Дb
SerProLysAsnAlaValProProValIleHisSerProAsnAspHis 251		233	Ş
GAACTTAAATATGAAGGAAAACTTGTAAGACGAACAACTGAATTGAAA 675		628	Db
TyrProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLys 232		213	γQ
AAAGGAAATGCTCTTCTGATCCAAGAAGTTCAAGAAGAAGATGGAGGAAATTACACATGT 627	AAAGGAAATG	568	Дb
AsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCys 212		193	Ş
CTGATGTTGTGTGGTATAAGGAATGCAAGCCAAAAATGTGGAGAAGCATAATAATACAG 567	CCTGATGITG	508	DЪ
ThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValllePro 192		173	Ş
ACTANAAGANAGGAGATCTCCTGTCCAGACATGGATGACTTTANAAAGTCCGATCAGGAG 507		448	Db
31nArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLys 172	IleG	155	Q.
TGCTACAACAGCAGGATCCGCTATTTAGAAAAATCTGAAGTC 447		406	DЬ
SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154		137	γ
:::         ::: :::    	TCAACATATTGCAT	346	рь
YşSerLyşValAlaPheProLeuGluValValGlnLysAspSer 136		119	δ
ATATGGTTTCACTCAGCTGAGGCACAAGACAGTGGATTCTACACTTGTGTTTTAAGGAAC 345		286	망
ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsn 118		99	Ş
TIGGAAGAGCCCATCATCTTTTCAGAGGTCAGGATGAGCAAAGAGAGAAGATCA 285		232	DЬ
ProlleAsnPheArgLeuProGluAsnArqIleSerLysGluLysAspVal 98		79	γQ
AGCACGGCCCAGAGCACTGGGCTCAGGCTTATGTGGTACAAAAACAAAGGTGAT 231		178	Db
TrpThr		59	Ş
GCAGGTGAACCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTAT 177		118	ДĎ
ProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyr 58		39	γQ
CTTTCAGTGGATGGCTGGATTGACTGGTCAGTGGATCTCAAGACATACATGGCTTTG 117		61	Db.
31uArgCyeAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPhe 38		20	Ş
:::         CTCACACTATTAGTGTCACACAATGCTCACTGTATGCTTATACCTCTTCTGATTTT 60		7	ф
LeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAsp 19	MetThrLeuL	<sub>L</sub>	S S

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US-10-011-548-34
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                                                                                                                                                                                                                                                                                        Sequence 34, Application US/10011548
Publication No. US20030055218A1
PUBLICANTION:
APPLICANT: Timans, Jacqueline
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                491
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAGGGGGCCTGGGAGCAATCTTCCTCCTCCTTGTACTGCTGGTGGTCATTTACAAATGC 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ÀAACATGCCAGTGTTTTGCTGCGTAAAAAGGATTTAATCTATAAAATTGAGCTT
                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValValLeuSerPro 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGlyGlyAsnThr---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACAACATTGAATTGATGCTCTTCTACAGGCAGCACTTTGGAGCTGATGAAACTAATGAT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValValTyrHisVal 380
                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                 CACTTAGTATATGAAATGCCCATCAAG 1665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAAGATCTCACAAGATATGTTGAACAAAGCAGAGACTTATTATCGTGCTAACTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTATGGATATAAACTCTTCATCCCAGAAAGAGACCTGATTCCAAGTGGAAGTGCATAC 1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGACAATCCTGAAGAAGAGCAGTTTGCTCTTGAAGTACTGCCAGATGTCCTGGAAAAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAACAAGGAATATGATGCCTATCTCTTACACAAAAGTGGACCAAGATACTTTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProHisProGly---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AsnSerIleAlaThr------LysLeuIleValValGluTyrArgProLeuGluHis 507
                                                                                                                                                                                                                                                                                                                                                                                                                               AlaLeuArgLeuAlaLeuProLeuArg 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACTATATTCTCAGACGGGGATGGAGTATT-----TTCGAACTGGAAAGCAGACTCCAT 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerPheValSerTrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLys 538
                                                                        STATE: California COUNTRY: USA
                                                                                                   STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                     ADDRESSEE: DNAX Research Institute
                                                            ZIP: 94304-1104
                                                                                                                                                                                               OF INVENTION: Human Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GGGAAAGTGAATTGCCAGGAAGTGGAATCACTAAAGCGTAGCATCAAACTT 1578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnAlaGluGluGluFheValLeuLeuThrLeuArgGlyValLeuGluAsn 431
                                                                                                                                                                                                                                                                           Timans, Jacqueline C.
Debets, Johannes Eduard Maria
                                                                                                                                                                                                                                            Antonius
Sana, Theodore R
                                                                                                                                                                                                                            Bazan, J. Fernando
                                                                                                                                                                                                             Kastelein, Robert A.
                                                                                                                                                                                 Methods
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                                                                                                                                                                                                  Proteins; Related Reagents
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . No.:
      298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
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US-10-061-727-2 (1-687) x US-10-011-548-34 (1-2537)
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                                  124 LysValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsnSerPro
                                                                                                                                                                                                                                                                                                                                                                                     44 ArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAlaHisSer 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 CysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluProAla 43
                                                                                                                                                                                                                                                                                                       64 AlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGluGluProIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..2004
SEQUENCE DESCRIPTION: SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCACTGACTGGTCTATCGAT---ATCAAGAAATATCAAGTTTTTGGTGGGAGAGCCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: line MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   CGAATCAAATGTGCACTCTTTTATGGTTATATCAGAACAAATTACTCCCTTGCCCAAAGT
                                                                                                                    ThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer 123
                                                                                                                                                                       GCCTTT-----GACGGAAGTAGAATGAGCAAAGAAGAAGACTCCATTTGGTTCCGGCCA
                                                                                                                                                                                                              AsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPheArgPro 103
                                                                                                                                                                                                                                                              GCTGGACTCAGTTTGATGTGGTACAAAAGTTCTGGTCCTGGAGACTTTGAAGAGCCAATA
AAAGTATCCATCTCACTGACAGTGGGTGAAAATGACACTGGACTCTGCTATAATTCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/011,548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/078,008 FILING DATE: 12-MAR-1998 APPLICATION NUMBER: US 60/081,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/173,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/065,776 FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/078,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 2537 base
                                                                                    ACAGGACAGTGGTCTCTACGCCTGTGTCATCAGGAACTCCACTTACTGTATG
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767.00
47.13%
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20.90%
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Matches:
Conservative:
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274
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•	41 AspArgAspSerLeuProGlyGlyAsnThrValGluAlaValPheAspPheIleGlnArg 46	) 음 용 성
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	293ThrileAspValThrileAsnGluSerIleSerHisSerArgThrGluAsp 309	B 8
	76 SerargAsnGluValTrpTrpThrIleAspGlyL	, B 3
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•	38 Lys 25 CTC	ξ.
	218 GlųAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerPro 237	음 성
	rPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValVa ;;:            TATAAGAGAAGTCAGAGAAGATGACATTGGAAATTATACCTGTGAATT	8 8
	178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnAs	, B &
	400 ATTTCATGCCGTGACATAGAGGATTTTCTACTGCCAACCA	, B 2
	142 MetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArg 1	S B S

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APPLICANT: REAL, SHATEDING.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FO)

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FO)

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FO)

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILLS OF INVENTION NUMBER: US/09/864,761

CURRENT FILLING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILLING DATE: 2000-05-26

PRIOR FILLING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: US 60/23,366

PRIOR FILLING DATE: 2000-09-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PILLING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00664
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APPLICANT: Rank, David R
APPLICANT: Hanzel, David
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FILING DATE:

2001-01-30

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OTHER INFORMATION: MAP TO AC008249.14

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1;
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.8;
OTHER INFORMATION: EST HUMAN HIT: BE892231.1, EVALUE 0.00e+00;
OTHER INFORMATION: NT HIT: AF167336.1, EVALUE 0.00e+00;
OTHER INFORMATION: SWISSPROT HIT: Q02955, EVALUE 7.00e-03;
US-09-864-761-32830
                                             RESULT 8
US-09-981-421-3
; Sequence 3, Application US/09981421
; Patent No. US20020098185A1
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GENERAL INFORMATION: APPLICANT: Sims, John APPLICANT: Mohler,
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LENGTH: 287
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APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00670
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APPLICATION NUMBER: PCT/US01/00662
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TITLE OF INVENTION: METHODS FOR TREATING IL
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
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TYPE: DNA
ORGANISM: Homo
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LOCATION: (1)...
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                                                                                                                                                                                                                                                                                                                                                                   GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTATCTGAAACATTGC
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                        GlyMetAsnLeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysVal
                                                                            IleThrTrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGlu---
                                                                                                                                     IleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr
                                                                                                                                                                                                                                                  TyrCysSerLysValAlaPheProLeuGluValValGln-----LysAspSerCysPhe
                                                                                                                                                                                                                                                                                TTTTGGCCAGTTGAATGACACAGGATCTTACTTTTTCCAAATGAAAAATTATACT
                                                                                                                                                                                                                                                                                                                                                                                               CATGAGATTGAAAACAACCACCAAAAAGCTGGTACAAAAGCAGTGGATCACAGGAACATGTG 198
                                                      -TCATTGTATAAGAACTGTAAAAAGCTACTACTGGAGAACAATAAAAACCCAACGATA
                                                                                                                                                                                                                                                                                                                                       -CAGATAACCTGTGAAAAC-----AGTTACTATCAAACACTGGTCAACAGCACA
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1162 GAAAATGGAGGAGCACACCTTTGCTGTGGAGATTTTTGCCCCAGGGTGTTGGAGAAACAT 1221
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                                                            LysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAlaLeuProLeuArgSerLeu 549
                                                                                                                                                                                                                                                                           ATGTCTAATGAGGTCAGGTATGAACTTGAAAGTGGACTCCATGAAGCATTGGTGGAAAGA 1401
                            CTTTCTTATAACTCAAGGTTCTGGAAGAACCTTCTTTACTTAATGCCTGCAAAAACAGTC
                                                                                                                                                      ProGlyIleLeuGlnLeuLysGluSerValSerPheValSerTrpLysGlyGluLysSer 529
                                                                                                                                                                                                                                  SerileAlaThrLysLeuIleValValGluTyrArgProLeuGluHisProHis-----
                                                                                                                                                                                                                                                                                                                  ValThrGluLysSerIleSerMetLeuGluPheLysLeu---GlyValMetCysGlnAsn 491
                                                                                                                                                                                                                                                                                                                                                                GAAATCCACTCACTGATAGAGAAAAGCCGAAGACTAATCATTGTCCTAAGTAAAAGTTAT
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                                                                                                               CCCCAATCACTAAAGCTTTTGAAATCTCACAGAGTTCTGAAGTGGAAGGCCGATAAATCT
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                                                                            US-10-061-727-2 (1-687) x US-10-157-447-1 (1-1626)
                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                 Query Match:
                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                      Alignment Scores:
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INFORMATION FOR SEQ ID NO: 1:
                                4 LeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAlaSerGluArg 23
                                                                                                                                                                                                                                                                                                              LOCATION: 1..57
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE: <Unknown-
APPLICATION NUMBER: 09/110,618
FILING DATE: <Unknown-
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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IMMEDIATE SOURCE:
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LENGTH: 1626 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
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COMPUTER READABLE FORM:
MEDIUM TYPB: Floppy disk
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    CTTTGGGTGCTTATATCTGTA--
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TITLE OF INVENTION: Receptor Designated
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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LOCATION:
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LOCATION:
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OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Vo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: WA
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ATCTTGGTGAGAAAAGCAGACATGGCTGATATCCCAGGCCACGTCTTCACA 984	934 ATCTTGGTG	문
alLysGlnLysValProAlaProArgTyrThrValGluLeu 360	346 LysValLys	Ş
CTAAATGTTTTATATAATTGCACTGTGGCCAGCACGGAAGGCACAGAAAAGCTTC 933	874 CTAAATGTT	망
ysArgSerTyrValCysHisAlaArgSerAlaLysGlyGluValAlaLysAlaAla 345	326 LeuLysArg	ঠ
a	814 CCAGAAGGC	뮹
GlnIleLeuSerIleLysLysValThrSerGluAsp 325	314	δ
CATGAAGAGAAAATGAGAATTATGACT 813	781 ATA	뮹
IleAspValThrIleAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThr	294 IleAspVal	Ş
TGAATGAAGAGGATGTAATTTATTGGATGTTTGGGGAAGAA	721 CTGAATGAA	
spSerArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThr 293	274 MetAspSer	Ş
GTGGAATTAGGAAAAAAGGTAAGGCTCAACTGCTCTGCTTTG 720	679 GTGGAATTA	
luLysGluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeu 273	254 TyrGluLys	₽.
GTGGAAGATCGCAGTAATATAGTTCCGGTTCTTCGGACCAAAGCTTAACCATGTTGCA 678	619 GTGGAAGAT	
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leThrTrpTyrMetG1yCysTyrLysileG1nAsnPneAsnAsnVallIeProglu 193	н	
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<pre>IleGlnArg leThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr 174 :::                                  </pre>	155 IleGlnArg	8
	13	Db 3
AsnSerProMetLysLeuProValHisLysLeuTyrIleGluTyrGly 154	139 Asn	Qy
AAATGGAAATTAAATGTCATCAGAAGAAATAAACACAGCTGTTTC 360	313 CAG	В 3
TyrCysSerLysValAlaPheProLeuGluValValGlnLysAspSerCysPhe 138	121 TyrCysSer	Qy J
PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120	101 PheArgPro	\$
CTGAACCCAAGGAGTTCCTCGAGAATTGCTTTTGCATGATTGTGTTTTGGAG 252	199 GAGCTG	망
GluProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrp 100	81 GluProIle	δ
HISSERALAGLYLEUTHILEUIIETFIYTIPHITAEGUHHABAHGYABHEUSHU OO	62 HisserAla     139 CATGAGATT	음 성
TGTACTTCACGTCCCCACATTACTGTGGAGGGGAACCT 105		Db
pAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGluPro 42	24 СуяАврАвр'	ঠ

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Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard
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1402 AAAATT-----AAAATGATTGAATTTGACACCTGTTACTGACTTCACATTCTTG 1455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 ---AspAlaGluGluGluGluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGlu 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            473 ValThrGluLysSerIleSerMetLeuGluPheLysLeu---GlyValMetCysGlnAsn 491
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                                                                                                                          CURRENT APPLICATION DATA:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

SOFTWARE: PStentin Release: #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
Methods
                                                   APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCCAATCACTAAAGCTTTTGAAATCTCACAGAGTTCTGAAGTGGAAGGCCGATAAATCT
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CITY: Palo Alto
STATE: California
APPLICATION NUMBER: 09/173,151
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sana, Theodore R.
Bazan, J. Fernando
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antonius
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                                                                                                                                                 Version #1.30
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (650) 852-9196
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
            532
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FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
AAGATGATTTTAGAAGTTAAGCCCCAGACAAATGCATCCTGTGAGTATTCCGCATCA---
                             LysValAlaPheProLeuGIuValValGlnLysAspSerCysPheAsnSerProMetLys 143
                                                               GGGTCATATATTTGTAGACCCCAAGATGATTAAGAGCCCCTATGATGTAGCCTGTTGTGTC
                                                                                        GlyAsnTyrThrCys-----MetLeuArg-----AsnThrThrTyrCysSer 123
                                                                                                                                  ---CACATCATCAGGACAAATGTACCCTTCACTTTTTGACCCCAGGGGTGAATAATTCT
                                                                                                                                                                AsnArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
                                                                                                                                                                                                                                 TrpTyrTrpThrArgGlnAspArgAspLeuGluGluPro]leAsnPheArgLeuProGlu 89
                                                                                                                                                                                                   TGGTACCAACAACCTTCGAATGGAGATCCATTAGAGGACATTAGGAAAAGCTATCCT---
                                                                                                                                                                                                                                                                                                                                   GATTTACCAGAGCCACAGAAATCACATTTCTGCCACAGAAATCGACTCTCACCAAAACAA 306
                                                                                                                                                                                                                                                                                                                                                                                                      ACAAAAAAACTCCTTTGGACATATTCTACAAGGAGTGAAGAGGAATTTGTCTTATTTTGT
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|TATTTCTTTGGCTTGTTGCAGGA-GAGCGAATTAAAGGATTTAATATTTCAGGTTGTTCC 186
                                                                                                                                                                                                                                                                                                                                                                          ProLeuPheGlu------HisPhe----
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LOCATION: 109..1905
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
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TTGAGCCCCAACTATGTCAATGGACCCAGTATCTTTGAACTACAAGCAGCAGTGAATCTT 1608
                                  LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal 487
                                                                        GGAGTGTATGCAGAAGACATTGTGAGCATTATTAAGAGAAGCAGAAGAGGAATATTTATC
                                                                                             GlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValVal 467
                                                                                                                                             GTTTTAGAAAACAAATATGGATATAGCCTGTGTTTGCTTGAAAGAGATGTGGCTCCAGGA 1488
                                                                                                                                                                             ValLeuGluAsmGluPheGlYTYrLysLeuCysIlePheAspArgAspSerLeuProGly 447
                                                                                                                                                                                                                                                                                                               CCAAGTGAGGCCACTTCATCTCTGAGTGAAGAACACTTGGCCCTGAGCCTATTTCCTGAT 1428
                                                                                                                                                                                                                                                      -----AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGly
                                                                                                                                                                                                                                                                                            ACGCTTGGGGÁTAAAÁAGGATTTTGÁTGCTTTCGTÁTCCTÁTGCAAAATGGAGCTCTTTT
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NAME/KEY: CDS
LOCATION: (484)..(2283)
COTHER INFORMATION:
US-10-212-287-6
US-10-061-727-2 (1-687) x US-10-212-287-6 (1-2681)
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                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 6
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CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: PCT/US99/01420
PRIOR FILING DATE: 1999-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Born, Theresa
TITLE OF INVENTION: ACPL DNA and Polypeptides
FILE REFERENCE: 2872-US
                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
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RESULT 12
US-09-981-421-1
Sequence 1, Application US/09981421 Patent No. US20020098185A1 GENERAL INFORMATION:
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AACACAACCCAGTCCGTCCAACTGAAAGAAAAG------AGAGGAGTGGTGCTC 1563
                                                                                                                                                               CysLysProValProGlnGluSerGluThrGlnTrpIleGlnAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TrpLysGlyGluLysSerLysHisSerGlySerLysPheTrpLysAlaLeuArgLeuAla 543
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                                                                                                                                                                                                                         AGGCTGATAGGAAATTCAAAGAGTCTCCTG-----
                                                                                                                                                                                                                                                             HisLeuArgAsnLysSerArgAlaGluIleHisAsnGlnProGlnTrpGluThrHisLeu
                                                                                                                                                                                                                                                                                                            TT-GCTGGACAGAACTCACAGCTCTGTGTGTGTGTGTTC--
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                                                                                                                              CCAGCACCAAGCAAGCTTGATGGACAATGG-----AATGGG 2433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: CDS
; LOCATION: (484)..(2283)
; OTHER INFORMATION:
US-09-981-421-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-061-727-2 (1-687) x US-09-981-421-1 (1-2681)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS FILE REFERENCE: 3086-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu :::::: ::: :::
                                                                                              ValAspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGly-----
                                                                                                                                                                                                                                                                                                                                AsnArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109
                                                                CTCAGCTGCCAA----AGTGATGCACAAAGTCCAGCGGTAACCTGGTACAAGAATGGAAAA 1071
                                                                                                                                                                                    LeuProValHisLysLeuTyrIleGluTyrGly---IleGlnArgIleThrCysProAsn 162
                                                                                                                                                                                                                                           AAGATGATTTTAGAAGTTAAGCCCCCAGACAAATGCATCCTGTGAGTATTCCGCATCA---
                                                                                                                                                                                                                                                                                     LysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLys 143
                                                                                                                                                                                                                                                                                                                                                                        GlyAsnTyrThrCys-----MetLeuArg-----AsnThrThrTyrCysSer 123
                                                                                                                                                                                                                                                                                                                                                                                                                    --- CACATCATTCAGGACAAATGTACCCTTCACTTTTTGACCCCCAGGGGTGAATAATTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCCCTGAGCACCTGCCCTTCATGGGTAGTAACGACCTATCT-----GATGTCCAA 732
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Born, Teresa L.
                                                                                                                                                   -CATAAGCAAGACCTACTTCTTGGGAGCACTGGCTCTATTTCTTGCCCCAGT 1014
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523 2097	504 ProLeuGluHisProHisProGlyIleLeuGlnLeuLysGluSerValSerPheValSer !	용 성
503 2040 · ·	488 MetCysGlnAsnSerIleAlaThrLysLeuIleValValGluTyrArg :	8 8
487 1983	468 LeuSerProAspTyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyVal (	음 성
467 1923	448 GlyAsnThrValGluAlaValPheAspPheIleGlnArgSerArgArgMetIleValVal (	음 성
447 1863	428 ValleuGluAsnGluPheGlyTyrLysLeuCysIlePheAspArgAspSerLeuProGly (	용 성
427 1803	414AsnAlaGluGluGluGluPheValLeuLeuThrLeuArgGly 4	₽,
413 1743		유 성
397 1683	spGlu   ::: ATCAG	<u> </u>
377 <sub>.</sub> 1623	360 LeuAlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuIleValVal :	<u> </u>
359 1563		음 성
339 1515	320 LygValThrSerGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGly :	음 성
319 1455	301 SerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys : ::	유 성
300 1395	281 TrpTrpThr11eAspGlyLysLysProAspAsp11eThr11eAspValThr11eAsnGlu :	8.
280 1344		유 성
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240 1230	221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla : :::::::::::::::::::::::::::::::::::	음 성
220 1170	201 IleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 2	용왕
1116	1072 CTCCTCTCTGTGGAAAGGAGCAACCGAATCGTAGTGGATGAAGTT	문

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; TYPE: DNA; ORGANISM: Homo s; PEATURE: CDS; NAME/KEY: CDS; LOCATION: (557).
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Patent No. US2002015526A1
GENERAL INFORMATION:
APPLICANT: Busfield, Samantha J.
TITLE OF INVENTION: NOVEL SECRETED IMMUNOMODULATORY PROTEINS AND USES THEREOF FILE REFERENCE: 0734-320001
CURRENT APPLICATION UNMBER: US/09/731,449
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
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                                695 GATTTTACCAGAGCCACAGAAATCACATTTCTGCCACAGAAATCGACTCTCACCAAAACAA 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlnSerSerGluArgAlaAlaGlySerPro-----ProAlaProGly***MetSerLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATTTTTCAGTGGAAAGGACTCAGTAGAACAGAAACCACTGGGAAGCAGCT-CCCAGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGGAATGGTGAAATGAGCCCTGGAGCCCCCTCCAGTCCAGTCCCTGGG---ATAGAGATG
                                                                     ProLeuPheGlu----
                                                                                                        ACAAAAAACTCCTTTGGACATATTCTACAAGGAGTGAAGAGGAATTTGTCTTATTTTGT 694
                                                                                                                                     ThrMetArgGlnIleGlnValPhe-----GluAspGluProAlaArgIleLysCys 47
                                                                                                                                                                           TATTTCTTTGGCTTGTTGCAGGA-GAGCGAATTAAAGGATTTAATATTTCAGGTTGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----CCAGCACCAAGCAAGCTTGATGGACAATGG-----AATGGG 2433
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-LeuLysPheAsnTyrSerThrAlaHisSerAlaGlyLeuThrLeuIle 69
                                                                                                                                                                                                                                                                                                8.13e-47
495.00
44.85%
26.42%
13.49%
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Matches:
Conservative:
Mismatches:
Indels:
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. <b>Q</b>	B 8	ß &	B 8	용 성	Dъ	} 8	B 8	용 성	d VQ	B &	P 64	Db .	. ∤ &	. B. 8	음 성	P &	B 8	Db
398	Qy 378 TyrHisValTyrTrpLeuGluMetValLeuPheTyrArgAlaHisPheGlyThrAspGlu :::	Qy 360 LeuAlaCysGlyPheGlyAlaThrValLeuLeuValValIleLeuII 	Qy 340 GluValAlaLysAlaAlaLysValLysGlnLysValProAlaProArgTyrThrValGlu :::::: :::::  :::	320 LysValThrS          1529 AAAGTCACTC	301 SerIleSer	281 TrpTrpThrIleAspGlyLys	Qy 261 GluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSerArgAsnGluVal	241 Val 1304 AAA	Qy 221 ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAla 	201 IleAla 1190	Oy 181 CysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPheLeu	163 ValAspGlyTyrPhe ::; 1088 CTCAGCTGCCAA	144 LeuProVal	Qy 124 LysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLys	Qy 110 GlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer	90 Asn 863	70 TrpTy       806 TGGTA	Db 755 GTCCCTGAGCACCTGCCCTTCATGGGTAGTAACGACCTATCT
413	PheTyrArgAlaHisPheGlyThrAspGlu 397	.euValValIleLeuIleValVal 377        :::    TGGTGGCCGTGCTGGCGGCGAGTGCCCTC 1696	ysValProAlaProArgTyrThrValGlu 359	erGluAspLeuLysArgSerTyrValCysHisAlaArgSerAlaLysGly 339       :::   AGCGTGATCTTCGCAGGAAGTTTGTTTGCTTTGTCCAGAACTCCATTGGA 1588	-HisSerArgThrGluAspGluThrArgThrGlnIleLeuSerIleLys 319     ::             :: : :: :: :: :: :: :	LysProAspAspIleThrIleAspValThrIleAsnGlu 300 	erPheLeuMetAspSerArgAsnGluVal 280     	ProProVallleHisSerProAsnAspHisValValTyrGluLysGluProGlyGlu 260	alLysValValGlySerProLysAsnAla 240   ::   :: 1303	LeulleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsnGly 220	leProGluGlyMetAsnLeuSerPheLeu 200 :: :: ;: :: 1189	ProSerSerValLysProThrIleThrTrpTyrMetGly 180	HisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCysProAsn 162	ysAspSerCysPheAsnSerProMetLys 143	rgAsnThrThrTyrCysSer 123 :: HAGAGCCCCTATGATGTAGCCTGTTGTGTC 979	ArgIleSerLysGluLysAspValLeuTrpPheArgProThrLeuLeuAsnAspThr 109	TTrpThrArgGlnAspArgAspLeuGluGluProIleAsnPheArgLeuProGlu 89	  ACGACCTATCTGATGTCCAA 805

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US-09-731-175-3
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09731175
Patent No. US20020098168A1
GENERAL INFORMATION:
APPLICANT: Glorioso, Joseph C.
Evans, Christopher H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1937
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                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTMARE: PATENTIA RElease #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                           Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer for Studying and Treating
a Connective Tissue of a Mammalian Host
                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGACAGAACTCACAGCTCTGTGTGTGTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCTTGGATGATCAA---ACACTGAAACTCATTTTAATTAAGTTCTGTTACTTCCAAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGAATGGTGAAATGAGCCCTGGAGCCCCCTCCAGTCCAGTCCCTGGGATAGAGATGTTG 2405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATTTTTCAGTGGAAAGGACTCAGTAGAACAGAAACCACTGGGAGGAGCT-CCCAGCCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAGAGGCTTAAAATCAGTTCCTCCCAATTCTAGGTTCTGGGCCCAAAATGCGCTACCAC 2230
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APPLICATION NUMBER: US/09/731,175 FILING DATE: 05-Dec-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                           CITY: San Francisco
STATE: California
                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -AsnAlaGluGluGluPheValLeuLeuThrLeuArgGly 427
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                                                                           Version
                                                                           #1.30
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; SEQUENCE DESCRIPTION: /product= "mouse interleukin-1 receptor" US-09-731-175-3
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1782 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                  208
424 ACACAGGCCACCTTCCCA---CAGCGGCTCCACATTGCC---GGGGATGGAAGTCTTGTG 477
                                 140 SerProMetLysLeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThr 159
                                                                          364
                                                                                                             122
                                                                                                                                              304 GTACCTGCCAAGGTGGAGGACTCAGGATATTACTATTGTATAGTAAGAAACTCAACTTAC 363
                                                                                                                                                                               102 ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyr 121
                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GAGATTGACGTATGTACAGAATATCCAAATCAGATCGTTTTGTTTTTTATCTGTAAATGAA 165
                                                                                                                                                                                                                                                                                                                                                                            166 ATTGATATTCGCAAGTGTCCTTACTCCAAATAAAATGCAC-------
                                                                                                                                                                                                                                                             82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 018484-002280US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/685,212 FILING DATE: 23-JUL-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                        CCCATATCAGCGGAC---CGGGACTCCAGGATTCATCAGCAGAATGAACATCTTTGGTTT 303
                                                                                                                                                                                                                                                       ProIleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPhe 101
                                                                        TGCCTCAAAACTAAAGTAACCGTAACTGTGTTTAGAGAATGACCCTGGCTTGTGTTACAGC
                                                                                                 CysSerLysValAlaPheProLeuGluValValGlnLysAspSer-----CysPheAsn 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KBY: CDS
LOCATION: 46..1776
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 08/183,563
FILING DATE: 18-JAN-1994
APPLICATION NUMBER: US 08/381,603
FILING DATE: 27-JAN-1995
APPLICATION NUMBER: US 08/567,710
FILING DATE: 05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/924,777
FILING DATE: 2000-01-31
APPLICATION NUMBER: US 07/963,928
FILING DATE: 20-0CT-1992
APPLICATION NUMBER: US 08/027,750
FILING DATE: 08-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                             ----LysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61
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484.50
46.04%
25.80%
13.21%
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Matches:
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Indels:
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153
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490 1494	472TyrValThrGluLysSerIleSerMetLeuGluPheLysLeuGlyValMetCysGln :::  ::::  ::::::::::::::::::::::::::	음 성
1446		유 성
1386		유 성
438 1326	GluPheValLeuLeuThrLeuArgGlyValLeuGluAsnGluPheGlyTyrLysLeuCys	유성
418 1266		음 성
404 1206		유
386 1146		유 성
366 1086		음 성
346 1026		음 성
326 972		유 왕
307 912		음 성
295 852		유 성
275 816	etAsp	유 성
255 765	GA GA GA GA GA GA GA GA GA GA GA GA GA G	유 상
235 711		음 성
215 651	198 SerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThr	음 성
197 591	178 TyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeu	유 성
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'equence 3, Application US/09899980A Patent No. US20020058800A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3 ^{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 7853-158
CURRENT APPLICATION NUMBER: US/09/899,980A
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/560,639
PRIOR FILING DATE: EARLIER FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                   10-061-727-2 (1-687) x US-09-899-980A-3 (1-4989)
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APPLICANT: Leiby, K.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-899-980A-3
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TYPE: DNA
ORGANISM: Mus musculus
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                                       226 AGTATTCCTACTCAA---AAAAGAAATCGGATCTTTGTCTCAAGAGCATCGTCTGAAGTTT 282
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                                                                                                                                                                                                                                                                                               22 GluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAspGlu 41
                                                                                                                                                                                                                                                                                                                                                67
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ArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyr 121
                                                                                                                                             HisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGluGlu 81
                                                                                                                                                                                            GCTTTAATTGTGAGATGCCCC----
                                                                                                                                                                                                              ProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThrAla 61 ::::::||||||
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                                                                        ProlleAsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPhe 101
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                                                                                                              ------TATCCTGTGGAATGGTATTACTCA------GATACAAATGAA 225
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419 GluPheValLeuLeuThrLeuArgGlyValLeuGluAsmGluPheGlyTyrLysLeuCys
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                                                                                                                 407 IleTyrValSerTyrAlaArg---------AsnAlaGluGluGlu 418
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                                                                     GCGTACATCATTTACCCTCGGGTCTTCCGGGGCAGCGCGGCGGGAACCCACTCTGTGGAG
                                                                                                                                                                                                   LeuPheTyrArgAlaHisPheGlyThrAspGluThrIleLeuAspGlyLysGluTyrAsp 406
                                                                                                                                                               CTGTTCTGGAGAGATATAGTGACACCTTACAAAACCCGGGAACGATGGCAAGCTCTACGAT 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGAATATGACTGTCTGGCCCTGAACCTTCATGGCATGATAAGGCACACCATAAGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----IleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThr 174
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Minimum
Maximum
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-MODEL-frame+_P2n.model -DEV=xlh
-MODEL-frame+_P2n.model -DEV=xlh
-Q-[cgn2 1/USPTO_spool/US10061727/runat_23042003_083116_7900/app_query.fasta_1.839
-DB=EST_-QFMT=fastap_-SUFFIX=rst_-MINNATCH=0.1_TCOPCL=0_-LCOPEXT=0
-UNITS-bits -START=1 -END=-1 -MRTRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=Ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10061727_@CGN_1 1 1456_@runat_23042003_083116_7900 -NCPU=6 -ICPU=3
-NO_XLPXY_NO_MAAP_-LARGEQUERY_NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOPP=10 -XGAPDEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Listing first 45 summaries
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Fgapop 6.0,
Delop 6.0,
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3669
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Result. ĕ. 570.5 569 625 602.5 587 817 807.5 805 784 536 497.5 497.5 494.5 488.5 700 687 685.5 685 675 876 873.5 Score Match 35.0 35.0 34.0 34.0 35.0 36.0 Length 910 580 596 598 598 598 533 643 814 723 756 888 643 멂 BM760155 AA237107 AI529899 AA107505 AI303998 AA571281 AA239486 ij BB644209 AW485290 T85756 AL544533 AW211290 BF237012 BI346913 BC016141 **180590** T08277 SUMMARIES BG032519 602301430 BI872969 603398140 AW427989 64724 MAR T70863 9415£12.r1 H80590 yu76e04.r1 BI065233 pgf1n.pk0 BI106737 602891267 AI529899 u183g06.y BB644209 BB644209 AW485290 64805 MAR BI065068 pgfin.pk0 AA819412 UI-R-AO-b BI340158 365346 MA T08277 EST06168 In BM751599 K-EST0027 BG711109 pglin.pk0 AV654169 AV654169 BB625831 BB625831 AA239486 mw98902.r BB6528271 BB6528271 BB653335 BB653335 AA107505 mp05d08.r BF237012 602026645 BB612046 BB612046 AL544533 AL544533 AA571281 v190903.r AV661936 AV661936 BB623025 BB623025 BQ561650 H4071F02-BB633613 BB633613 BE892231 601435065 BI346913 376288 MA AV656295 AV656295 BM760155 K-EST0040 AW211290 uo79b07.y AI303998 ui63d12.y BI331848 602982528 AA237107 mw96b02.r AV659167 AV659167 AL543511 AL5435: BI862501 60339 Description BC016141 Homo

## ALIGNMENTS

AUTHORS TITLE	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BC016141	RESULT 1
Strausberg,R. Direct Submission	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1549)	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens.	HTC.	BC016141.1 GI:16359373	BC016141	IMAGE:3920152, mRNA.	Homo sapiens, interleukin 1 receptor accessory protein, clone	BC016141 1549 bp mRNA linear HTC 24-OCT-2001		

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COMMENT
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Query Match:
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PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mENA gi: 4504660
This clone has the following problem: frame shifted.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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/db_xref="LocusID:3556"
/db_xref="taxon:9606"
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/clone_Tib="NIH_MGC_72"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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AL543511
                                                Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                      Homo sapiens
                                                                         Contact: Genoscope
                                                                                       Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 849)
                                                                                                                                                                                                            AL543511
AL543511.1
                                                                                                                                                                                                                                     AL543511 LTI_NFL006_PL2
prime, mRNA sequence.
                                                                                                                                                         Eukaryota; Metazoa;
                                   segref@genoscope.cns.fr,
                       Location/Qualifiers
/organism="Homo
                                                                                                                                                                                                              GI:12875989
                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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sapiens cDNA clone
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ArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySerProLysAsn-Al
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                                                          ATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGA
                                                                                                                                       TGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGTASTGAACTTGAGTTTCCTC
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/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pCMVSPORT 6; Site_1 in NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com"
206 c 185 g 224 t 2 others
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| IleGluTyrGlyIleGlnArgIleThrCysProAsnValAspGlyTyrPheProSerSer
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                                                                     ValValGlnLysAspSerCysPheAsnSerProMetLysLeuProValHisLysLeuTyr
                                                                                                                                                                                           CGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCCGGCCCACTCTCCTCAATGACACTGGC
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1 (bases 1 to 873)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
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/db_xref="taxon:9606"
/clone="IMAGE:5399668".
/clone=lib="NHIM MGC_87"
/clone lib="NHIM MGC_87"
/lab_host="PH108 (phage-resistant)"
/lab_host="PH108 (phage-resistant)"
/note="Organ: breast; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally; oligo-dT primed. Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
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                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LINI at:
http://image.llnl.gov
Plate: LLAMI131 row: n column: 22
High quality sequence start: 3
High quality sequence start: 3
High quality sequence stop: 870.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (199)
Contact: Robert Strausberg, Ph.D.
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                  quality sequence start: 3 quality sequence stop: 870. Location/Qualifiers
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US-10-061-727-2 (1-687) x BI330085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGluGluProIleAsnPhe
GlyLysLysProAspAspIleThrIleAsp-ValThrIleAsnGluSerIleSerHisSe
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/db xref="taxon:10090"
/clone="IMAGE:5135061"
/clone="IMAGE:5135061"
/clone lib="WCI CGAP Li9"
/clone lib="WCI CGAP Li9"
/lab_host="DH10H (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: liver; Vector: pCMY-SPORT6; Site_1: NotI;
/note="Organ: liver; V
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UI-H-EI1-ayz-f-07-0-UI.s1 NCI_CGAP_EI1 Homo
IMAGB:5845638 3', mRNA sequence.
BQ006059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                     /note="Organ: Left Pelvis; Vector: pNTT3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI CGAP EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_EI1"
/tissue_type="Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:5845638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Homo.sapiens"/
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  4.91e-109
1124.00
99.53%
98.59%
30.64%
                                                                                                                                                                                              LIB=UI-H-EI1
TISSUE=chondrosarcoma
SEQ=ACACTTGCAC"
164 c 157 g 286
                      Length:
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                     AW211290 723 bp mRNA linear EST 03-DEC-1 u079b07.y1 NCI CGAP Mam3 Mus musculus cDNA clone IMAGE:2648725 similar to gb:X85999 M.musculus mRNA for interleukin 1 receptor accessory (MOUSE);, mRNA sequence.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                  Tumor Gene Index
Unpublished (1997)
                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                         TTTCTGGTÄGTGGTTCTCATTGTGGTTTACCÄTGTTTACTGGCTGGÄGÄTGGTCCTCTTT
                                                       LeuLeuValValI1eLeuI1eValValTyrHisValTyrTrpLeuGluMetValLeuPhe
                                                                                                             GlnLysValProAlaProArgTyrThrValGluLeuAlaCysGlyPheGlyAlaThrVal
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                                                                                              GAGAAAGTCATACCACCAAGGTACACAGTAGAACTCGCCTGTGGTTATGGAGCCACGGTC
                                                                                                                                                          AACTATGTCT
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                                                                                                                                                                                                                                                                                                             AATGACCGTGTTGTCTATGAGAAGAACCAGGAGAGGAACTGGTTATTCCCTGCAAAGTC 181
                                                                                                                                                                                                                                                                                                                                                                                      AsnAspHisValValTyrGluLysGluProGlyGluGluLeuLeuIleProCysThrVal
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/lab_host="D10B"
/note="^~~
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Location/Qualifiers
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/tissue_type="tumor, gross
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:2648725"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 314 200 1010
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Porest Park Parkway, Box 8501, St. La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina 1 (Dases 1 to 756)
1 (Dases 1 to 756)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dietrich,N., Dietrich,N., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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ui63d12.yl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1887095 5' similar to gb:X85999 M.musculus mRNA for
interleukin 1 receptor accessory (MOUSE);, mRNA sequence.
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                      Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."

185 c 167 g 195 t 10 others
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/clone lib="Sugano mouse liver
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN1132 row: h column: 08
High quality sequence stop: 802.
Location/Qualifiers
PheArgProThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThr 120
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NIH-WGC http://mgc.nci.nih.gov/.
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/clone="IMAGE:5135287"
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Mammalia; Butheria; Primates; Catarrhini; Hominidae;
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Tissue Procurement: ATCC/DCTD/DTP
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/clone="Ib="NMGE:3920152"
/clone_lib="NHH_MGC_72"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCWV-SPORT6; Site 1: N
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                                                                                                                                                                                   pig.
Sus scrofa
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376288 MARC
BI346913
USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, US Tel: 402 762 4366
                                        Design and use of two per discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                 Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Stone, R.T., Heaton, M.P., Grosse, W.M., Benne and Keele, J.W.
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                                                                                                                                        Mammalia; Eutheria;
1 (bases 1 to 580)
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                                                         AGCCCAGACTATGTGACAGAAAAGAGCATCAGCATGCTGGAGTTCAAGCTGGGTGTCATG
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PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.989904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACKWARD: GTTTTCCCAGTCACGACG
Plate: 130 row: L column: 3
Seq primer: ATTTAGGTGACACTATAG.
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l: smith@email.marc.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
/db xref="taxon:9823"
/clone_lib="MARC_2PIG"
/clsue_type="pooled"
/lab_host="DHIOB"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall;
/Inbrary made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
a 110 c 158 g 153 t
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GAGGAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAG
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                                                                           AlaValProProValIleHisSerProAsnAspHisValValTyrGluLysGluProGly
                                                                                                                   GGCTGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTC
                                                        Chinese National Human Geno
351 Guo Shoujing Road, Zhan
201203, p. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,Ş., Gu,W., Hung,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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AV656295
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: hanzg@chgc.sh.cn
This clone is available at CHGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV656295.1
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XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="GLCEPH02"
/clone lib="GLC"
/clone lib="GLC"
/tissue_type="corresponding
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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db_xref="taxon:9606"
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Primates;
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ne GLCEPH02 3', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: yongsung@mail.kribb.re.kr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 489) im, N.S., Hahn, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
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/note-rorgan: Stomach; Vector: pCNS; Site 1: EcoR1;
Site 2: Not1; The poly (A)+ RNA was decapped with tabacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoR1 site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoR1 which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F' by electroporation method.
After analyzing and sequencing about 2,000 ~ 3,000
colonies in original cDNA library, the abundant cDNAs were
selected and amplified by PCR reaction using vector region
primer including T7 promotor as 5' primer and N (dT)14 as
3' primer. The PCR products were used as template for
synthesis of biotinylated single stranded RNA by in vitro
transcription reaction. The synthesized RNA probes were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Epithelial"
/cell_line="SNU-668"
/lab_host="Top10F'"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sex="M"
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clone="S2SNU668s1-14-A03"
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E., Sohn, H.Y., Kim, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp mRNA linear EST 04-MAR-2002 sapiens cDNA clone S2SNU668s1-14-A03
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Kim,J.M., Park
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158 þ hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells i coli Top10F' with electroporation method."

REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION RESULT 13 AA237107 BASE COUNT ORIGIN 밁 S 밁 S 닭 S В δ 밁 Ś 문 S 밁 S 밁 Ş 밁 Ś Pred. KEYWORDS DEFINITION US-10-061-727-2 (1-687) x BM760155 (1-489) Query Match: Best Local Similarity: Percent Similarity: Score: Alignment Scores: Shoor . No.: 483 317 423 363 303 24:3 237 183 297 277 257 217 123 197 177 157 63 w TrpTyrMetGlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsn ArgIleThrCysProAsnValAspGlyTyrPheProSerSerValLysProThrIleThr Serile ArgAsnGluValTrpTrpThrIleAspGlyLysLysProAspAspIleThrIleAspVal GluProGlyGluGluLeuLeuIleProCysThrValTyrPheSerPheLeuMetAspSer ProGluAsnGlyArgThrPheHisLeuThrArgThrLeuThrValLysValValGlySer LeuSerPheLeuIleAlaLeuIleSerAsnAsnGlyAsnTyrThrCysValValThrTyr AGCATC ACCATTAACGAAAGTATAAGTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTG ThrileAsnGluSerIleSerHisSerArgThrGluAspGluThrArgThrGlnIleLeu CGCAATGAGGTTTGGTGGACCATTGATGGAAAAAAACCTGATGACATCACTATTGATGTC GAACCAGGAGGAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCT CCAAAAAATGC ProLysAsnAlaValProProValIleHisSerProAsnAspHisValValTyrGluLys TGGTATATGGGCTGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAAC AGGATCACTTGTCCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACT CCAGAAAATGGACGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCT TTGAGTTTCCTCATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACATAT Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu (bases 1 to 598)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and AA237107 598 bp mRNA linear imw96b02.rl Soares mouse NML Mus musculus cDNA clone l similar to gb:X85999 M.musculus mRNA for interleukin accessory (MOUSE); mRNA sequence. EST Eukaryota; Metazoa; Mus musculus AA237107 house mouse. AA237107.1 488 318 6.07e-83 876.00 100.00% 100.00% 23.88% GI:1861163 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mismatches: Indels: Gaps: Length:
Matches:
Conservative: EST 03-MAR-1997 IMAGE:678507 5' Murinae; Mus. 1 receptor 482 316 236 182 196 422 296 362 276 302 256 242 216 122 62 176

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                                                                                                                                                                                                                                                                                                                   AsnPheArgLeuProGluAsnArgIleSerLysGluLysAspValLeuTrpPheArgPro 103
                                                                                                                   TTCCCAGTGCACAAGATGTATATTGAACATGGCATTCATAAGATCACATGTCCAAATGTA
                                                                                                                                    LeuProValHisLysLeuTyrIleGluTyrGlyIleGlnArgIleThrCysProAsnVal 163
                                                                                                                                                                                            LysValAlaPheProLeuGluValValGlnLysAspSerCysPheAsnSerProMetLys 143
                                                                                                                                                                                                                                                           ThrLeuLeuAsnAspThrGlyAsnTyrThrCysMetLeuArgAsnThrThrTyrCysSer 123
                                                                                                                                                                                                                                                                                                                                                           TCTGGCCTTACCCTGATCTGGTACTGGACCAGGCAAGACCGGGACCTGGAGGAGCCCATT 72
                 IleGlnAsnPheAsnAsnVallleProGluGlyMetAsnLeuSerPheLeuIleAlaLeu 203
                                                        GACGGATACTTTCCTTCCAGTGTCAAACCATCGGTCACTTGGTATAAGGGTTGTACTGAA
                                                                              AspGlyTyrPheProSerSerValLysProThrIleThrTrpTyrMetGlyCysTyrLys 183
ATAGTGGACTTTCATAATGTACTACCCGAGGGCATGAACTTGAGCTTTTTCATCCCCCTTG
                                                                                                                                                                              AAAGTTGCATTTCCCCTGGAAGTTGTTCAGAAGGACAGCTGTTTCAATTCTGCCATGAGA
                                                                                                                                                                                                                                                                                                   AACTTCCGCCTCCCAGAGAATCGCATCAGTAAGGAGAAAGATGTGCTCTGGTTCCGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smail: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
MGI:418211
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Fax: 314 286 1810
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Washington University School of MedicineP
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The WashU-HHMI Mouse EST Project
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146 c
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/clone="IMAGE:678507"
/clone_lib="Soares mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HisLeuThrArgThrLeuThrValLysValValGlySerProLysAsnAlaValProPro 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCATTGCCTTAATTTCAAATAATGGAAATTACACACATGTGTTGCTTACATATCCAGAAAAT 167
                 LeulleAlaLeulleSerAsnAsnGlyAsnTyrThrCysValValThrTyrProGluAsn 219
                                                          GGCTGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTC 107
                                                                           GlyCysTyrLysIleGlnAsnPheAsnAsnValIleProGluGlyMetAsnLeuSerPhe 199
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I (bases 1 to 789)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Zeguang Han
Chinese National Human
351 Guo Shoujing Road,
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV659167 GLC Homo sapiens
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                                                                                                                                                                                                                                                                                                           /note="Vector: pBluescript sk(-); Site_1:
XhoI"
                                                                                                                                                                                                                                                                                                                                         /tissue type="corresponding non cancerous liver tissue"
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/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                         clone_lib="GLC"
                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                       clone="GLCFUB08"
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863.00
97.09%
97.09%
23.52%
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Primates;
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308 3', mRNA sequence.
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RESULT 15
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ORGANISM
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Arakawa T. Carrinci, P., Fukuda, S., Furumo, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, P., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nonura, K., Ohno, M., Okazaki, Y., Oklo, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagamai, M., Tagawa, A., Takahashi, P., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
                                                                                                                                                   Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
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RÎKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Suc,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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RIKEN full-length enriched, adult male diencephalon Mus
CDNA clone 9330131B06 5', mRNA sequence.
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AlaHisSerAlaGlyLeuThrLeuIleTrpTyrTrpThrArgGlnAspArgAspLeuGlu GAGCCGGCTCGAATCAAGTGCCCCCCTCTTTGAACACTTCCTGAAGTACAACTACAGCACT GluProAlaArgIleLysCysProLeuPheGluHisPheLeuLysPheAsnTyrSerThr TCGGAGCGCTGTGATGACTGGGGACTAGATACCATGCGACAAATCCAAGTGTTTGAAGAT 252 SerGluArgCysAspAspTrpGlyLeuAspThrMetArgGlnIleGlnValPheGluAsp 40 AIGGGACTICTGTGGTATTTGATGAGTCTGTCCTTCTATGGGATCCTGCAGAGTCATGCT 192

80

312

372

60

193

133

21

373

432

US-10-061-727-2 (1-687) x BB625831 (1-652)

1 MetThrLeuLeuTrpCysValValSerLeuTyrPheTyrGlyIleLeuGlnSerAspAla

Percent Similarity: Best Local Similarity:

8.7e-81 858.00 94.22% 89.60% 23.39%

Length:
Matches:
Conservative:
Mismatches:

155 155 10 0

Gaps: Indels: Score: Pred. No.:

Query Match:

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Alignment
                                                                    BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                    153
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                                                                                                                                                                                                                                                                                                                                                                            /note-"Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diencephalon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="diencephalon"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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/clone="9330131B06"
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.rch completed: April 30, 2003, 12:17:45 Job time : 1684 secs

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Title:
Perfect score:
Sequence:
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16160.396 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 1 AR166115 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS		4.4 5.0	43	41	39 40	38	36	ມ ເປ 4. ປັ		31		2 2 8	26 27	25	223	. 22	20 21	19	1 <b>7</b>	16	C 14	13.	c 11	. 10	80	7 6	ហា៖	ωω	21	Result No.
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accessory proteins 28-AUG-2001;	1740 bp DNA E US 6280955.	ALIGNMENTS	AR102821 E26333	F167333S07	AR102826	AR102820 E26332	HSU43672	AR016447	MMU277831	AX410972	AF284437 C098400	AR179667	HSA243874 AR179677	AF284435	AF181284	HSA272208 AF284436	HSA290436	AF212016 F167333S08	AR179668	F167333S06 F167333S09	F167333S05	AC098400	AC008249	Ó	AK095107 AC108747	BC021159	RNU48592	MMIL1RACP	AB006537 AR166116	AR166115 AF029213	ID
, nucleic acids and	linear PAT 17-OCT-2001		E26333 Polypeptide	339	0282	AR102820 Sequence E26332 Polypeptide	72 Hu	6447	AJ277831 Mus muscu		7	67 Seque	Homo	AF284435 Homo sapi	Homo	AF284436 Homo sapi	90436 Homo	AF212016 Homo sapi AF167340 Homo sapi	9668 Seque	AF167341 Homo sapi	7337 Homo	AC098400 Rattus no	AC008249 Homo sapi	3 Mus n	AKU95107 Homo sapi AC108747 Homo sapi	9 · Mus	Arib/343 Homo Sapi U48592 Rattus norv	M. mus	AB006537 Homo sapi	115 Sequence 213 Homo sap	ripti

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	541 TGTTATAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTC 600	B 8
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	241 GAGCCAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAAGATGTGCTGTGG 300 	р 9
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	121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACA 180	B. 8
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AF029213
LOCUS
DEFINITION Homo sapiens IL-1 receptor accessory protein mRNA, complete cds.
ACCESSION AF029213
VERSION AF029213.1 GI:2599126
KEYMORDS
SOURCE
ORGANISM Homo sapiens.
CREATION Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS
TITLE
AUTHORS
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POOS. Natl. Acad. Sci. U.S.A. 94 (24), 12829-12832 (1997)
REFERENCE
2 (bases 1 to 1740)

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TITLE
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Direct Submission
Submitted (07-OCT-1997) Biology, Tularik, Inc.,
South San Francisco, CA 94080, USA
Location/Qualifiers
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IKCPLEHFLKENYSTRASAGLTLIWYMTRQDBDLEEPINFLERNISERGDVLWFR
PTLLNDTGNYTCYCHANFTYCSKVAFPLEVOVGNSCFNSPMKLPVHKLYIEVGIQAITC
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                                                                    GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACA
                                                     GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACA
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Mammalia; Eutheria;
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/product="interleukin 1 receptor accessory protein"
/product="interleukin 1 receptor accessory protein"
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/db_xref="rG1:3041773"
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IKCPLFEHFLKFNYSTAHSAGLTLIWYMTRQDRDLEEPINFRLPENKISKEKDVLWFR
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PNUDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPE
PTLANDTGNYTCHTWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPE
NGTFHLTRTLTVKVVGSPKNAVPFVIHSPNDHVYEKEFGEELLIPCTWFPSFLADS
RNEVWHTIDGKKGDITIDVINESIGHSRTBDETRTOILSIKKYESDLKRSYCHA
RSAKGEVAKAAKVKQKVPAPRYTVELACGFGATVLLVVILIVVYHVYMLEMVLFYRAH
FGTDETILDGKEYDITVSYARNAEEBEFVLLTLRGVLEMEFGYKLCIFDRDSLPGGIV
TDETLSFIQKSRRLLVVLSPNYVLGGTQALLELKAGLENMASRGNINVILVQYKAVKE
TKVKELKRAKTVLTVIKWKGEKSKYPQCRFWKQLQVAMPVKKSPRRSSSDEQGLSYSS
LKNV"
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/db_xref="taxon:9606"
/tissue_type="brain"
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207._.1919
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0; Mismatches 171;
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                                                                                                                        GATGGAAAGGAGTATGATATTTATGTTTCCTATGCAAGAATGTGGAAGAAGAGGAATTT
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Greenfeder c *
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Mammalia; Eutheria;
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/db_xref="MGD:MGI:104975"
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/translation="MGILWYLMSISFYGILQSHASERCDDWGLDTWRQIQVFEDEPAR
IKCPLFEHFLKYNVSTHASSGITLIWYMTRQDRDLEEFINFRLPENRISKEKDULWFR
PTLLNDTGNYTCMLRNTTYCSKVAPFDLEVVQKDSCFNSAMFPVHHOYIEHGIHKITC
PNUDGYFPGSSVFSVTWYKGCTEIUDFHNVLPFEGMNLSFFIPLVSUNGNYTCVUTYPE
NGRLFHLTRTVTVKVVGSPKDALPPQIYSPNDRVVYEKEPGEELVIPCKYYFSFIMDS
HNEVMWTIDGKKPDDVTVDITINESVSYSSTEDEFTNJLSIKKYTPEDLARNYVCHA
RNTKCEREQDAKVKOKVIPRRYTVELAGGFGATVFLVVLIVVHVYMLEMVLFYRAH
FGTDETILDGKEPDIYVSYARNVEEERFVLLTLRGVLENEFGYKLCIPDRDSLPGGIV
TDETISFIOKSRRILVVLSPNYVLGGTQALLELKAGLENAASRGNINVILVQYKANKD
                                                                                                                                                                                                                                                                         /db xref="taxon:10090"
/cell line="3T3-L1"
/clone lib="cpw"
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                                                            MKVKBLKRAKTVLTVIKWKGEKSKYPQGRFWKQLQVAMPVKKSPRWSSNDKQGLSYSS
LKNV"
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/protein_id="CAA59991.1"
/db_xref="GI:887521"
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                                                                                                  GTTACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGGGGAA
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                                                                                                                                                                                                                                                                                    Homo sapiens soluble interleukin-1 receptor (ILIRAP) mRWA, complete cds. AP167343.1 GI:8050486
                                              Submitted (08-JUL-1999) Department of Pharmacology, Uni
Pennsylvania, 156 Johnson Pavilion, 3420 Hamilton Walk,
Philadelphia, PA 19104, USA
Location/Qualifiers
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Jensen, L.E., Muzio, M., Mantovani, A. and Whitehead, A.S.
IL-1 signaling casecade in liver cells and the involvement
soluble form of the IL-1 receptor accessory protein
J. Immunol. 164 (10), 5277-5286 (2000)
                                                                                                Direct Submission
                                                                                                             Jensen, L.E.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Best Local Similarity
Matches 1051; Conserv
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                                                                             TGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTC
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/ db xref="GI:8050487"

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PTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITC
ENVDGYFPSSVKETITWYMGCYKIQNFNUT IPGMNLSFLIALISNNCHYTCVVTYPB
NGRTFHLTRTLTVKVVGSPKNAVPPVHRSNDIFYDSTALIPCTYYSFFLDS
RNEVMWTIDGKKPDDITIDVTINESISHSRTEDETRTQILSIKKVTSEDLKRSYVCHA
RSAKGEVAKAAKVKQKGNRCGQ"
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/codon_start=1
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1 (bases 1 to 1862)

Liu,C., Chalmers,D., Maki,R. and De Souza,E.B

Liu,C., Chalmers interleukin-1 receptor a

Rat homolog of mouse interleukin-1 receptor a

cloning, localization and modulation studies

Mauroimmunol. 66 (1-2), 41-48 (1996)
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mRNA, c
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Submitted (06-FEB-1996) Changlu Liu,
Biosciences, Inc., 3050 Science Park
Location/Qualifiers
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Eukaryota; Metazoa;
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                                            /codon_start=1
/product="interleukin-1 receptor accessory protein"
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PNVDGYFPSSVKPSVWYKGCTEIVNFHNVQPKGMNLSFFIPLVSNNGNYTCVTTYLE
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HNEIWWTIDGKKPDDVPVDITIIESVSYSSTEDETRTQILSIKKVTPEDLKRNYVCHA
RNAEGEAEQAAKVKQKVIPPRYTVELACGFGATVFLVVVLIVVYHVYWLEMVLFYRAH
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/db_xref="taxon:10116"
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                                                                                                                               GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT
                                                                                                                                                                                                                                       CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTTGGTATATGGGC
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AGTATAAGTCATAGTAGAACAGAAGAAGAACAAGAACTCAGATTTTGAGCATCAAGAAA
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                                                 TGGTGGACCATTGATGGAAAGACCTGATGACGTCCCTGTTGACATCACTATTATTGAA
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                                                                                                                                                                          GTACCACCTCATATCTACTCGCCAAATGACCGCGTTGTCTATGAGAAGGAACCAGGAGAG
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TDETLSFIQKSRRLLVVLSPNYVLQGTQALLELKAGLENMASRGNINVILVQYKAVKD
LKVKELKRAKSVLTVIKMKGEKSKYPQGRFMKQLQVAMPVKKSPRWSSDKQGLSYSS
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ATGACACTICIGIGGIGIGIGAGICAGAGICTCIACTITIATGGAAICCIGCAAAGIGATGCC ATGGGACTTCCTTGGTGTTTGATGAGTCTGTTCTTCTGTGGGATCCTGCAGAGTCACGCT 162 Similarity Conservative 50.9%; 78.2%; 0; Score Pred. Mismatches No. 2.6e 8; DB 10 2.6e-291; les 352; 10; Indels Length 1862; 6; Gaps 60 2;

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                                                           Submitted (07-JAN-2002) Nat
Gene Collection (MGC), Canc
Institute, 31 Center Drive,
                                                                                                                            Strausberg, R. -
                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
1 (bases 1 to 1916)
Strausherr P . .
                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                    BC021159.1
Email: cgapbs-r@mail.nih.gov
              NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                                                                                                                       house mouse.
                                                                                                         Direct Submission
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                                                          ) National Institutes of Health,
Cancer Genomics Office, National
rive, Room 11A03, Bethesda, MD 20
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CCCATGAAACTCCCAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTTGT
                                    TACTGCAGCAAAGTTGCATTTCCCCCTGGAAGTTGTTCAGAAGGACAGCTGTTTCAATTCT
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6680420.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton,
Madan, Stephanie Rodrigues, Amy Sanchez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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/db_xref="GI:1808148"
/db_xref="GI:18088148"
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PTLANDTGNYTCMLRWTTYCSKVAFPLEVVQCDSCFWSAMR PPUHKWYIEHGHIKITC
PNVDGYFPSSVKPSVTWYKGCTEIUDFHNVLFEGMALSFF!PILVSNNGNYTCVTTYPE
NGRLFHITRTWTVKYVGSFKDALPPQIYSPNDRVVYEKEBGEELVIPCKVYFSFIMDS
MRELFHITRTWTVKYVGSFKDALPPQIYSPNDRVVYEKEBGEELVIPCKVYFSFIMDS
HNEUWWTIDKKEPDVTVDITINESVSYSSTEDETRTQILSIKKVTPEDLRRNYVCHA
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399 c 420 g 503 t
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/clone_lib="NCI_CGAP_Li9"
/lab_host="DH10B"
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/product="Similar to
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db_xref="taxon:10090"
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                                                                               Kodaira, H., Puruya, T., Takahashi, M., Kikkawa, E., Omura, Y., Abe, K. Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai Hio, Y., Saito, K., Nishikawa, T., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kiwuchi, H., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                   AK095107.1 GI:21754300
Oligo capping; fis (full insert sequence).
Homo sapiens hippocampus cDNA to mRNA, clone_lib:BRHIP2
clone:BRHIP2028593.
    2 (bases 1 to 2226)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) T.
                                                                   Nagahari, K., Masuho, Y., Nac
NEDO human cDNA sequencing
                                                                                                                                                                                              Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T.,
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  (04-JUL-2002) Takao Isogai,
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="GI:21754301"
/tamslation="MIVUSPDYVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLEH
/translation="MIVUSPDYVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLEH
PHPGILQLKESVSFVSMKGEKSKHSGSKFWKALRLALPLRSLSASSGMNESCSSQSDI
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46509 bp DNA linear PRI 21-JUN-2002
Homo sapiens 3 BAC RP11-268E23 (Roswell Park Cancer Institute Human
    2 (bases 1 to 46509)
Worley, K.C.
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| (bases 1 to 46509)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,

Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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Submitted (31-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are o sequenced and submitted once, so the sequence for the remainder the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STSs are identified using ePCR (Genome of a local database that includes entries
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Baylor Plaza, Houston, TX 77030,
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                                                                                /rpt_family="AluSq"
complement(1457. .1
                                                                                                                                                                                                                                                                                    complement(321. .613)
/rpt_family="AluSx"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 function="clone overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="overlaps bases 182198. .184202 of clone AC008249"
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'chromosome="3"
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        family="L1M4"
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and Lander, E.

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

Birren, B.,

Linton, L., Nusbaum, C.,

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Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Kamat, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Submitsion Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (25-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the record
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L25964
Center clone name: 345_H_5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is updated, the accession number will
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37694 36159 23015 16995 35336 3905 14004: gap of 1 4005 14727: contig of 12277 12376: gap of 1 40103: 1 40203: gap 19735: gap of 100 b 20454: contig of 719 20554: gap of 100 b 21277: contig of 723 18079: gap of 18803: con 17256: gap of 100 b 17979: contig of 723 32047: gap of 100 k 32769: contig of 722 28794: gap of 100 bp 29511: contig of 717 bp 16456: gap of 1 17156: contig of 11552: gap of 12276: con 39400: 37793: 36994: 36158: 35335: 33682: 32869: 31215: 30395: 29611: 23844: gap of 24571: con 23014: gap of 100 l 23744: contig of 730 21377: gap of 18903: gap of 15642: 14827: 13211: gap of 38609: 27968: 27145: 26321: 25483: 24671: 22196: gap of 34407: 7 33582: ~ 31947: 31115: cont 15542: con-ຈບຯ: gap 39300: c 38509: cont 35235: contig of 728 335: gap of 100 k 36058: contig of 723 11: gap of 100 b 30295: contig of 684 21: gap of 100 p 27045: contig of 724 22914: 11452: contig 37693: 13904: 36894: 27868: 26221: contig of 738 03: gap of 40929: con 28694: 22096: 19635: 16356: gap of gap of gap of gap of gap of 83: contig of gap of 1 gap of gap of contig of 723 contig of 714 contig of 693 contig of contig of 703 contig of 699 contig of 736 contig of 713 contig of 720 contig of 726 contig of contig of contig of contig of 732 contig of 724 contig of contig of 732 œ, of 723 100 bp 100 bp 100 bp 100 bp 100 bp of 732 bp in length 100 bp f 703 bp in length dq 001 100 bp 718 719 700 715 712 đđ ď ďq ď đđ ď g bp in length gd ď bp in length å bp in length bp in length bp in length bp in length 'n in length length

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GAGGGCTGCAGGCCCTCCAGCCCCAGGCNCAATGTCCAAGCACCGAGGGAAGTCCTC
                                                                             GGATCACGTTCAAAGGAGGAGAAGTCGTTTGAAAGAGCCCCCAGAACTTCAGAGCTCAGA
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45955 46680; contig of 726 bp in length
46681 46780; gap of 100 bp
46781 47505; contig of 725 bp in length
47506 47605; gap of 100 bp
47606 48321; contig of 716 bp in length
48322 48421; gap of 100 bp
48422 49134; contig of 713 bp in length
49135 49234; gap of 100 bp
48978; contig of 74b bp in length
49979 50078; gap of 100 bp
50079 50806; contig of 728 bp in length
50907 50906; gap of 100 bp
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53282: contig of 729 bp in length
53283
53382: gap of 100 bp
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54104: contig of 722 bp in length
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54204: gap of 100 bp
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54923: contig of 719 bp in length
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55753: contig of 730 bp in length
754
55853: gap of 100 bp
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56576: contig of 723 bp in length
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56676: gap of 100 bp
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45854: contig of 694 bp in length
45954: gap of 100 bp
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43411: contig of 716 bp in length

43511: gap of 100 bp

44234: contig of 723 bp in length

44334: gap of 100 bp

443360: contig of 726 bp in length
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42595: contig
42695: gap of
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Pred. No. 8.7e-137;
D; Mismatches 88;
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AGCCAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                Submitted (09-JUL-1999) Department of Pharmacology, University Pennsylvania, 156 Johnson Pavilion, 3620 Hamilton Walk, Philadelphia, PA 19104, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              Jensen, L.E.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jensen, L.E., Muzio, M., Mantovani, A. and Whitehead, A.S. IL-1 signaling cascade in liver cells and the involvem soluble form of the IL-1 receptor accessory protein J. Immunol. 164 (10), 5277-5286 (2000)
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537. .822
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T VAL	TA TARGE A	PRS CE L	ICE DRS	13 10N 10N	62 34	14 02 74
Direct Submission Submitted (16-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  '5' (bases 1 to 184203) Worley,K.C. Direct Submission Submitted (21-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 28, 1999 this sequence version replaced gi:6091634. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu	Direct Submission  Submitted (30-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  (bases 1 to 184203)  Worley, K.C.  Direct Submission  Submitted (28-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  (bases 1 to 184203)	Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucier, R., Martin, R., Martinez, C., McLeod, M. P., Mei, G., Moore, S., Moorish, T., Morgan, M., Morris, S., Nash, S., Nelson, A., Nguyen, R., Nguyen, N., Nguyen, S., Oswal, G., Parish, B., Paxton, S., Payron, B., Perez, L., Pu, L. L., Quiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R., Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Naylor, S.L., Nelson, D. and Gibbs, R. Direct Submission L Unpublished 2 (bases 1 to 184203)	Eukaryota; Metazoa; Chordatá; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 184203)  Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Budota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Frantz, P., Ganesh, R., Garcia, D.K., Gorrell, J.H., Guevara, W., Harris, K., He, X., Hernandez, J., Budoson, L. P., Hollows, C., Hogar, H., Garcia, D.K., Gorrell, J.H., Guevara, W., Harris, K., He, X., Hernandez, J., P., Hollows, C., Hogar, H., Forcon, L. P.	pp DNA 3 (Roswell	ATTG 365	

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice sites that maintained sequence continuity across the splice sites that maintained sequence

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at TRL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT------

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# bases		Position 6949 148395 171291 171310	Contig length: Phrap values i Phrap values i Phraction of Ph Praction of Ph Number of cons Number of N's
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	ibution	Consensus changing Original+Context aaggagactg(n)acaactcttt tctattattg(n)tttattctct gagagaágaa(n)caactgacta taaggcatga(n)agcaattagg	- Summan estimat ate (BCA ap value change change change change change)
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		ctcttt ttctct tgacta attagg	-05

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Phrap Value

25 30 Range

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FEATURES
Query Match 14.2%; Score 292.8; DB 9; Best Local Similarity 97.7%; Pred. No. 1.4e-72; Matches 297; Conservative 0; Mismatches 7;
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complement (11066...11420)
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complement (11691...11844)
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14723...14817
                                                                                                                                                                                                                                                                                                                                               /rpt_family="(TA)n"
complement(10047..10329)
/rpt_family="L1MB8"
complement(10336..10618)
/rpt_family="L1M4"
                                                    /rpt_family="MER20"
complement(17300..17452)
/rpt_family="L2"
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/rpt_family="L1MB8"
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complement(15958..16174)
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RESULT 14 AC098400/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REPERENCE AUTHORS	Oy 62 0  Db 153275 0  Qy 122 2  Db 153335 4  Db 153395 0  Qy 182 0  Db 153395 0  Qy 242 4  Db 153455 4  Db 153515 7  Qy 362 4  Db 153575 0	3
ACO99400 87015 bp DNA linear HTG 31-JUL-2002 (CON Rattus norregicus clone CH230-2B16, *** SEQUENCING IN PROGRESS ***, 49 unordered pieces.  NA CO99400.2 GI:21953618  ROC99400.2 GI:21953618  ROC99400.2 GI:21953618  ROC99400.2 GI:21953618  ROC99400.2 GI:21953618  ROC99400.2 GI:21953618  RACUSS PHANEL:  I (bases I to 87015)  RATTUS  RATTUS  I (bases I to 87015)  RADNIA, J., Banchon, J., Binage, K., Blankenburg, K., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Barks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonkia, D., Burket, C., Re, J., Chacko, J., Chavez, D., Chen, R., Dathorne, S. R., David, R., Davila, M. L., Davis, C., Dern, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Ding, Y., Dinh, H. H., Delaney, K. R., Dejado, O., Denn, A. D., Dedarich, D. A., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Frantz, P., Garza, M., Hallton, K., Gill, R., Garza, M., Marinale, A., Martinez, B., Hamiton, R., Gill, R.	CAGAACGCTGCGATGACTGGGACTACACCATGAGGCAAATCCAAGTGTTTTGAAGTG 121	

Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (31-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 24, 2002 this sequence version replaced gi:16328167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-OCT-2001) of Molecular and Human (Baylor Plaza, Houston, (bases 1 to 87015)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                 NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                          be preserved
                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 45081 bases at least Q40
Consensus quality: 48248 bases at least Q30
Consensus quality: 50450 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 87015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: CH230-2B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: TUPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                             2 (bases 1 to 548)
Dale, M., Cox,A. and Nicklin,M.J.H.
Direct Submission
Submitted (28-JUL-1997) Department of Molecular and Genetic Medicine, University of Sheffield, Royal Hallamshire Hospital, Sheffield S10 2JF, United Kingdom
On Feb 26, 1998 this sequence version replaced gi:2909774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens interleukin-1 receptor accessory protein (ILIRAP) APO16261
                                                                                                                                                                                                                                                                                                                                                                   The human gene encoding the interleukin-l receptor accessory protein (ILIRAP) maps to chromosome 3q28 by fluorescence in situ hybridization and radiation hybrid mapping Genomics 47 (2), 325-326 (1998)
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/note="RPCII PAC library; Ioannou,P.A. and de Jong,P.J.,
Construction of bacterial artificial chromosome librarie
using a modified pl (PAC) system, Current Protocols in
Human Genetics Unit 5.15, 1996"
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/clone="CH230-2B16"
15816 c 15778 g 229
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/db_xref="taxon:9606"
/chromosome="3"
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ob_xref="taxon:10116"
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                          AAACCGACTATCACTTGGTATATGGGCTGTTATAAAATACAGAATTTTAAT 564
                                                      TATATTTCTTTTTCAGGAACACTACATATTGCAGCAAAGTTGCATTTCCCTTGGAAGTT 293
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/gene="IL1RAP"
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/gene="IL1RAP"
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<251. .>437
                                                                                                                                                                                                                                                                                                                                                                                              /product="interleukin-1 receptor accessory protein"
/protein id="AAC39609.1"
/db_xref="GI:2909775"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="cytokine receptor co-receptor"
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30, 2003, 09:15:23

Search completed: April Job time: 4260 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1385.2
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/SIDS2/gcgdata/geneseq/
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AAA09048
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/geneseg/genesegn-embl/NA1981.DAT:*
/geneseg/genesegn-embl/NA1982.DAT:*
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Human interleukin-
Human interleukin-
Soluble interleukin-
Fusion polypeptide
Mouse interleukin-
Mouse interleukin-
Human interleukin-
Probe #14473 for g
Probe #18472 used
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89.6 89.6	95 95 95	95			o o	113.6	139.4	142	142	•	145.2	145.2	146	149	149	149	149	149	149	149	149	149	151	151	164.2	220	220
4.4. 	444	4.6	4.6	4.6			•	•		7.0	7.0	7.0		7.2	•		7.2	7.2	7.2	7.2	7.2	7.2	7.3	7.3	8.0	10.7	10.7
1626 1626 1626	400 400	400	400	400	229	443	1737	3120	3120	2537	3122	2091	1979	169	169	169	169	169	169	169	169	169	2061	2061	246	478	478
18 20 24	22 22 24	222	222	22	21	24	20	22	22	24	22	21	20	24	22	22	22	22	22	22	22	22	24	20	24	22	22
AAT88774 AAX87651 AAD31175	AAI35857 AAI04308 ABS04460	AAK29896 AAI14482	ABA25860 AAK04398	ABA56209	AAC09103	ABN97121	AAX58247	AAK52925	ABA09029	AAD27179	AAK51941	AAA27919	AAX84308	ABS16980	AA109300	AAI48995	AAI23682	AAK42922	AAK17135	ABA35757	ABA68793	ABA50826	AAD27170	AAX58245	ABN18246	AAI36611	AAI15283
Human receptor pro Human interleukin- Human IL-18 recept	Probe #4543 used to Probe #4299 used to Human genome-deriv	#4415 for	Probe #4326 for ge Human brain expres		Human secreted pro	Gene #3619 used to	Human IL-IRD8 codi	Human polynucleoti	_	-	polyn	-	-	-	#9291	#17681 used		bone m	brain e	•		Human breast cell	Human interleukin-	Human IL-1RD8 codi	Human ORFX polynuc	Probe #5297 used t	for 9

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## ALIGNMENTS

RESULT 1 AAS15608

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16-DEC-1997;
                                                                       28-AUG-2001.
                                                                                                                                                      Homo sapiens
                                                                                                                                                                     IL-1R acP; human; interleukin-1 receptor accessory protein; NF-kappaB;
IL-1; IL-1RI; ss; inflammatory response.
                                                                                                                                                                                                                 21-MAY-2002 (first entry)
                                                                                                                                                                                                                                   AAS15608;
                                                                                                                                                                                                                                                 AAS15608 standard; cDNA; 1740 BP
                                                                                            US6280955-B1
                                         16-DEC-1997;
                                                                                                                                                                                               Human interleukin-1 Receptor accessory protein (IL-1R acP) cDNA.
                        (TULA-) TULARIK INC
                                        97US-0991944
                                                          97US-0991944.
                                                                                                            /product= *IL-1 Receptor accessory protein*
                                                                                                                            Location/Qualifiers
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Best Local Similarity
Matches 1517; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involving NF-kappaB in a cell may be achieved by modulating the activity of II-1RAcp using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant II-1RacP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic II-1RacP nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active II-1RacP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the human interleukin-1 receptor accessory protein (IL-IRacP) cDNA of the invention. The interleukin receptor accessory protein (IL-IRacP) and its modulators (agonists) are useful for regulating cell function. Transient expression of either IL-IRI or IL-IRacP alone does not result in ligand-independent induction of an NF-kappaB dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-IRI and IL-IRACP as a result of protein overexpression can elicit a signaling pathway leading to NF-kappaB activation. Modulation of signal transduction in the continuous activation of signal transduction is a cell of the continuous activation of signal transduction is continuous.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GAGCCAGCTCGCATCAAGTGCCCACTCTTTGAAACTCTTTGAAATTCAACTACAGCACA 180
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                          CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC 540
                                                                                                                      CCCATGAAACTCCCAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTTGT 480
                                                                                                                                                                                 TATTGCAGCAAAGTTCCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCC
                                                                                                                                                                                                                TATTGCAGCAAAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTTCAATTCC 420
                                                                                                                                                                                                                                                                                                                      TTCCGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACA 360
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CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC
                                                                                         CCCATGAAACTCCCAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTTGT
                                                                                                                                                                                                                                                                               TTCCGGCCCACTCTCCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide (IL-1RacP) to a binding target.
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89.6%;
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Pred. No. 0;
0; Mismatches 171;
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1558TCTTTTGTGAGCTGGAAGGGAGAAAGTCCAAACATTCTGGCTCTAAATTCTGGAAA 161	B 정
1498 GTTGAGTACCGTCCCCTTGAGCACCCGGCACCCAGGCATTCTTCAGCTCAAAGAGTCTGTG 15	유 성
1441 CTGGAGTTTAAACTGGGTGTCATGTGCCAGAACTCCATTGCCACCAAGCTCATTGTG 14	β Q
1381 AGCAGAAGATGATTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAGAGCATCAGCATG 14	B 8
1321 GACCGAGACAGTCTGCCTGGGGGAAATACAGTGGAAGCAGTTTTTGATTTCATTCA	B 8
1261 GTATTACTGACCCTCCGTGGAGTTTTGGAGAATGAATTTGGATACAAGCTGTGCATCTTT 13 	DP Q2
01 GATGGAAAAGAGTATGATATTTATGTATCCTATGCAAGGAATGCGGA 	DB 92
1141 TACTGGCTAGAGATGGTCCTAFTTTACCGGGCTCATTTTGGAACAGATGAAACCAFTTTA 12	DP 64
1081 GCTTGTGGTTTTGGAGCCACAGTCCTGCTAGTGGTGATTCTCATTGTTGTTTACCATGTT 11	B 8
1021 GTTGCCAAAGCAGCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTG 10 	B &
61 GTTACCTCTGAGGATCTCAAGCGCAG( 	pb Qq
901 AGTATAAGTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAA 96 	B 8
41 TGGTGGF         50 TGGTGGF	B 8
781 GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT 840	P &
721 GTGCCCCTGTGATCCATTCACCTAATGATCATGTGGTCTATGAGAAAGAA	P &
661 CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA 7	B 84
TACATATCCAGAAAAT              ACATATCCAGAAAAT	B 6
ATACCCGAAGGTA             ATACCCGAAGGTA	B &

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RESULT 2
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AC AAT3
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                                                                                             Query Match
Best Local Similarity
Matches 1515; Conserv
                                                                                                                                                                                 A cDNA clone (AAT32026) codes for human interleukin-1 receptor accessory protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind to or otherwise activate the IL-1R. esp. the Type 1 IL-1R. It was obtd. from a human YT cell cDNA library using a probe derived from a human partial genomic clone. The cDNA can be used for the prodn. of pure IL-1R AcP by expression in a host cell. The IL-1R AcP is used to treat or prevent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1675
                                                                                                                                                                                                                                                                                                              prods. to treat or prevent of interleukin-1
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                                                                                                                                                                                                                                                                                     Claim 2; Page 71-72; 115pp; English.
                                                                                                                                                                                                                                                                                                                          Isolated interleukin-1 receptor accessory protein - used to develop prods. to treat or prevent inflammatory or immunological activities
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                                                                                                                                                Sequence 1713 BP;
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                                                             ATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAGTGATGCC
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           TCAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCCAAGTGTTTTGAAGAT 120
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                                                ATGACACTTCTGTGGTGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAGTGATGCC
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                                                                                                Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A CDNA clone (AAT32027) codes for a soluble form (AAW01912) of the human interleukin-1 receptor accessory protein (IL-1R AcP), a protein that inhibits the ability of IL-1 to bind to, or otherwise activate IL-1R, esp. the Type 1 IL-1R. It was obtd. by PCR amplification (see also AAT32029-30) of cDNA (AAT32026) coding for extracellular domain of IL-1R AcP (AAW01911). The soluble protein was expressed in Sf9 insect cells using a baculovirus system. It can be used to treat or prevent the inflammatory or immunological activities of IL-1, and also to screen for IL-1 antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated interleukin-1 receptor accessory prods. to treat or prevent inflammatory or of interleukin-1
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This sequence encodes fusion polypeptide 569, which is capable of binding cytokine IL-1 to form a non-functional complex. The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine; binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta signal transducing component causing beta-receptor dimerization, the soluble alpha specificity determining component of the receptor (sR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine by binding the cytokine to form heterodimers (sR-alpha:beta-1) that act as antagonist to the cytokine by binding the cytokien to form a non-functional complex. The receptor components are shared by cytokines such as the CNTF (ciliary)
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A cDNA clone (AAT32028) codes for mouse interleukin-1 receptor accessory protein (II-IR AcP), a protein that inhibits the ability of II-1 to bind to, or otherwise activate, the II-IR, esp. the Type 1 II-IR. It was obtd. by screening cell-surface proteins in COS-7 cells transfected by 3T3-II cDNA using anti-murine II-IR ACP monoclonal antibody 4C5, and isolation of cDNA clones from positive lines. The murine cDNA was used to obtain a partial genomic clone of the human homologue. A probe derived from this genomic clone was then used to isolate the full-length cDNA (AAT32026) for human II-IR AcP (AAW01911).
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CC coexpression of both proteins resulted in a 20-fold increase in a cativation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-IRI and IL-IR AcP as CC a result of protein overexpression can elicit a signaling pathway CC leading to NF-kappaB activation. Modulating signal transduction CC involving NF-kappaB in a cell may be achieved by modulating the activity CC of IL-IRAcp using binding agents such as agonists and antagonists. CC Hybridisation probes to the CDNA sequence can be used to identify wild-CC type and mutant IL-IR AcP alleles in clinical and laboratory camples. Mutant alleles are used to generate allele-specific CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses CC of diseases or disorders with an inflammatory response. In therapy, therapeutic IL-IRAcp nucleic acids are used to modulate cellular expression or intracellular concentration or availability of cative IL-IR AcP. This invention also comprises a method of screening for a part that the content also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for a contive IL-IR AcP. This invention also comprises a method of screening for the continuation of the continuation of the continuation of the continuation of the continuation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the mouse interleukin-1 receptor accessory protein (IL-IR AcP) cDNA that was used to generate a cDNA fragment used as a hybridisation probe to isolate, from a cDNA library the human IL-IR AcP cDNA of the invention. The interleukin receptor accessory protein (IL-IR AcP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-IRI or IL-IRAcP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however the property of the
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P-PSDB; AAU09967.
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                                                                                                     agent that modulates the interaction of an interleukin receptor cessory polypeptide (IL-1R AcP) to a binding target.
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Sequence 3355 BP; 909 A; 742 C; 753 G; 951 T; 0 other;

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This cDNA clone codes for human interleukin-1 receptor accessory

molecule (IL1-R AcM) (see AAW33897), a new member of the

immunoglobulin superfamily that forms a complex with type 1 IL1-R

and which has higher affinity for IL-1 than the receptor itself,

suggesting that the known high and low affinity forms of IL1-R are

in fact the receptor with or without IL1-R AcM, respectively.

The 2155 bp sequence is present in clone HMEBIS2 (deposited as

C ATCC 97666) derived from microvascular epithelium (no details of

isolation given). Recombinant expression in Escherichia coli,

mammalian and insect cells is described. Recombinant host cells

and recombinant vectors are claimed. Also claimed are isolated

nucleic acid molecules encoding epitope-bearing portions (see

AAW5398-9.15) of IL1-R AcM. Recombinant I1-R AcM can be used to

identify IL-IR agonists and antagonists useful for therapeutic

modulation of IL1-B acM, antagonists useful for trarapeutic

Nucleic acid fragments are useful as diagnostic probes and primers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Interleukin-1 receptor accessory molecule; IL-1R AcM; human; signal transduction; infection; septic shock; inflammation; rheumatoid arthritis; therapy; ds.
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P-PSDB; AAW53897.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding interleukin-1 receptor accessory protein used for therapeutic modulation of IL-1 activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bednarik DP,
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303..1373
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Best Local S
Matches 1049
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les 1049; Conserv
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                                                                                      CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAAIGCA 720
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AGTATAAGTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAA
                                            TGGTGGACCATTGATGGAAAAAAACCTGATGACACTATTGATGTCACCATTAACGAA
                                                                           GAGCTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTT
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Pred. No. 0;
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CAGCTCGCATCAAGTGCCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGCCC 184 AACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATGAGC

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Query Match Best Local S Matches 287

13.9%; Score 287; DB 22; al Similarity 100.0%; Pred. No. 7.7e-81; 287; Conservative 0; Mismatches 0;

Length Indels

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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                               The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format, directly from WIPO
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                                                                                                                                                                                analyzing
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cervical cancer; ss.
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                                                                                                                                                           Claim 25;
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30-JUN-2000;
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                      specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                     2001-488901/53.
                                                                                                                                                                                genome-derived single zing gene expression in
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                                                                                                                                                          SEQ ID No 14473; 487pp; English.
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                                                                                                                                                                                                                                                                                          ; 2000US-0180312.
; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
; 2000GB-0024263.
BP;
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76 A; 78 C;
                                                                                                                                                                                                                                              Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression analysis in human cervical cell sample.
                                                                                                                                                                                    'n
                                                                                                                                                                                                                                              Ξ
                                                                                                                                                                                                                                                                      INC
                                                                                                                                                                                    exon nucleic acid probes useful
n human cervical epithelial cell:
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 68 G;
                                                                                                                                                                                                                                              Rank
  65 T; 0 other;
                                                                                                                                                                                                                                              DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epithelial cell;
                                                  of the printed
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                                        from WIPO
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RESULT 9
AAI49786
ID AAI4
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                                                                              Query Match
Best Local Sim:
Matches 287;
                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312.

26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.

04-OCT-2000; 2000GB-0024263.
                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
                                                                                                                                 Sequence 287 BP; 76 A; 78 C; 68 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human placenta -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder; ss
                                                                                                                                                                                                                                               Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157272-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe #18472 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2001
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 125
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                                                                              Local Similarity 100.0%; Poses 287; Conservative 0;
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CAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGCCC 184
                                       AACGCTGCGATGACTGGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTTGAAGATGAGC 124
                                                                                                                                                                                                                                                                                                                                           SG,
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                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                            SEQ ID No 18472; 654pp; English.
                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                         13.9%;
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                                                                           Score 287; DB 22;
; Pred. No. 7.7e-81;
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RESULT 10
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26-MAY-2000; 2000US-0207456.

30-JUN-2000; 2000US-0608408.

03-AUG-2000; 2000US-0632366.

21-SEP-2000; 2000US-0234687.

27-SEP-2000; 2000US-0236359.
                       expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene
                                                                                                                                                                                               Claim
                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                         WPI; 2001-488901/53.
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                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
                                                                                                                                                                                            SEQ ID No 5216; 487pp; English.
                                                                                                                                                                                                                                                                                                     Hanzel DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression analysis in human cervical cell sample
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Query Match
Best Local Similarity
Matches 220; Conserva

Conservative

10..0%; Pr 100.0%; Pr

Score 220; DB 22; pred. No. 2.8e-59;

Length Indels

478;

Mismatches

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Gaps

0;

Sequence

478 BP; 139 A; 105 C; 112 G; 122 T; 0 other;

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                                                       Query Match
Best Local Similarity
                                                                                                         The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders.
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26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder;
                                                                                      Sequence
                                                                                                                                                                                                                                        WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probe; microarray; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe #5297
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                                                                                                                                                       The present invention relates to single exon nucleic acid probes (SENP)
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CAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATG
                     CAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful zing gene expression in human placenta -
                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS INC
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234589.
2000US-0234359.
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                                                     10.7%;
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                                           0;
                                                     Score 220; DB 22;
Pred. No. 2.8e-59;
                                                                                        112
                                                                                                                                                                                                                                                             Rank DR;
                                          Mismatches
                                                                                                                                                                              English
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RESULT 12
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                                                                           ireating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic transplantation, cardiovascular diseases, diabetes mellitus, systemic manufacture beneficially hyperparative diabetes mellitus, systemic
                                                                                                                                                                                                                   The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Tab) in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000;
29-AUG-2000;
                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID 4969; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Novel human polypeptides and polynucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shimkets RA,
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                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABP02494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-MAY-2001; 2001WO-US10836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ORFX polynucleotide sequence SEQ ID NO:4969
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2000US-228716P.
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                                                                                                                                                                                                                                                                                                                                                                        autoimmune
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transplantation, Cardiovasculla Laure, you cholesterol ester lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host arthritis, autoimmune inflammatory eye disease. ORFX proteins are also

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RESULT 13
AAX58245
ID AAX58
XX AAX58
XX AAX58
XX AAX58
XX L22-JU
DT 22-JU
XX L1-1-1
KW IL-1-1
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Best Local Simi
Matches 193;
                                                                                                                                                                     17-NOV-1997;
12-MAR-1998;
18-MAR-1998;
15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reperfusion injury in various tissues systemic cytokine damage.
N.B. The sequence data for this paren
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating burns, incisions, ulcers, for treating osteopor bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-1RD9; IL-1RD8; IL-1RD10; interleukin-1; IL-1receptor DNAX; therapy; IL-1 receptor-like protein; abnormal expression; immunological disorder; inflammatory disorder; morphological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
   Interleukin-1
                                     P-PSDB;
                                                           WPI; 1999-326545/27.
                                                                                              Bazan
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15-OCT-1997;
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                                                                                                                                 SCHERING
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                                     AAY14128.
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                                                                                            Debets JEMA,
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 receptor-like
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98US-0040714.
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polypeptides
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Pred. No. 1.2e-41;
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   RD8,
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This sequence encodes a interleukin-1 (II-1) receptor-like polypeptide, designated II-1 receptor DNAX designation 8 (II--IRDB), of the invention. The II-IRDB, II-IRDB, and II-IRDD proteins, their fragments and muteins, also related antibodies, other binding agents and (ant) agonists are used to treat conditions associated with abnormal expression of the polypeptide or abnormal expression of, or response to, their ligands, e.g. immunological, inflammatory or morphological disorders. They may also be used to screen for binding agents (potential drugs), diagnostic reagents (to detect the proteins or their ligands) and to isolate related sequences. Antibodies may also be used to raise anti-idiotypic antibodies, as carriers for toxins, radiomuclides or other
Sequence 2061 BP; 656 A; 421 C; 459 G; 525 T; 0 other;
                                                                                                                        therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 28; Page 93-96; 150pp; English
                                                                                                                  agents, and for affinity purification.
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DB 20;

Length

6

Matches Query Match Best Local Similarity 317 731 677 617 611 557 551 497 491 437 431 377 371 311 263 251 209 149 131 191 92 71 32 11 TGTGGTGTAGTGAGTCTCTACTTTTATGGAATCCTGCAAAGTGATGCCTCAGAACGCT ATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCAGTGCCCCCTG TTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGACGTTCC TACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTCATTGCCTTAA ATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGCTGTTATAAAA TCCCAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTTGTCCAAATGTAG AGGTGTCAATGTCCTTGACTGTTGCAGAGAATGAATCAGGCCTGTGCTACAACAGCAGGA AAGTTGCATTTCCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCCCCCCATGAAAC CTGAGGCACAAGACAGTTGTACACTTGTGTTTTTAAGGAACTCAACATATTGCATGA CTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACATATTGCAGCA TCTTT----TCAGAGGTCAGGATGAGCAAAGAGGAAGATTCAATATGGTTTCACTCAG ACTTCCGCCTCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCCGGCCCA CTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGGACCTTGAGGAGCCAATTA GAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTATAGCACGGCCCAGAGCA GCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGCCCATTCAG GCATTGACTGGTCAGTGGATCTCAAGACATACAT---GGCTTTGGCAGGTGAACCAGTCC GCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATGAGCCAGCTC TCTGTTCTGTAGTCAGCACAAATCTGAAGATGGTGTCAAAGAGAAATTCTGTGGATGGCT TGGAGAATCAGCCAAGTGTTATAGATGTCC CAACTGAATTGAAAGTTACAGCTTTACTCACAGACAAGCCTCCCAAGCCATTGTTCCCCA **AAGAAGATGGAGGAAATTACACATGTGAACTTAAATATGAAGGAAAACTTGTAAGACGAA** AAATGTGGAGAAGCATAATAATACAGAAAGGAAATGCTCTTCTGATCCAAGAAGTTCAAG ATGACTTTAAAAAGTCCGATCAGGAGCCTGATGTTGTGTGGTATAAGGAATGCAAGCCAA TCCGCTATTTAGAAAATCTGAAGTCACTAAAAGAAAGGAGATCTCCTGTCCAGACATGG CTGGGCTCAGGCTTATGTGGTACAAAAACA-----AAGGTGATTTGGAAGAGCCCATCA 697; Conservative 7.3%; 47.4%; 0; Score 151; DB 20; Pred. No. 8.5e-37; Mismatches 715; Indels 57; Gaps 790 730 676 670 616 610 556 550 496 490 436 430 376 370 316 310 262 250 208 190 148 91 736 70

AGCTGGGTAAGCCTCTGAACA

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RESULT 14
AAD27170
ID AAD27
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AC AAD27
XC AAD27
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DT 09-A)
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DE Huma
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17-NOV-1997;
12-MAR-1998;
18-MAR-1998;
15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mammalian physiology such as morphogenesis of immune system function. The invention particularly relates to nucleic acids, proteins and antibodies which regulate development and/or the immune system. The invention also relates to antibody fragments which specifically bind to antigenic fragments of a primate interleukin (IL)-1 receptor like molecules such as IL-1 receptor DNAX designation (IL-IRD). The antibody fragments of the invention are useful to treat conditions exhibiting abnormal expression of the receptors or their ligands which typically will be immunological disorders. The present sequence is a DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody fragments which specifically bind to primate interleukin receptor-like molecules are useful to treat conditions associated abnormal expression of the receptor or its ligand, particularly immunological disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 11-16; 102pp; English.
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                                                            AAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCCCCCATGAAAC
                                                                                                                     CTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACATATTGCAGCA
                                                                                                                                                                                             ACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCCGGCCCA
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    TCCCAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTTGTCCAAATGTAG
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GACGGGGATGGAGTATTTTCGAACTGGAA 1470
                                                                  CAAGATATGTTGAACAAAGCAGAAGACTTATTATCGTGCTAACTCCAGACTATATTCTCA 1441
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RESULT 15 ABA50826 .ID ABA50826 standard; DNA;

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                                                                                                                                                                                                                                                                         nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label developed from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for centrying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical agents on cells. The microarray of this invention presents a far greater diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The Drister sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                               Best Local Similarity
Matches 149; Conserv
                                                                                                                                                                                                                Query Match
                 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
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27-SEP-2000;
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TGCCAAAGCAGCCAAGGTGAAGCAGAAAG
                                                                    TACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCGAAGT 1022
                                                                                                                TATAAGTCATAGTAGAACAGAAGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAAGT 60
                                                  TACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCGAAGT
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; 2000US-0632366.
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2000US-0236359.
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Db 121 TGCCAAAGCAGCCAAGGTGAAGCAGAAAG 149

Search completed: April 30, 2003, 08:04:12 Job time: 328 secs

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Perfect score:
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ore greater than or equal to the score of the result being printed,
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1: /cgn2_6/ptodata/1,

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US-09-032-337-42

US-09-032-337-38

US-09-560-639-3

US-09-560-639-4

US-08-381-603-1

US-08-924-376-1
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US-08-996-338-7

US-08-996-338-2

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US-08-991-944-3

US-09-173-151A-3

US-09-173-151A-34
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38	38	39.4	39.4	39.4	41.6	41.6	43	49.4	49.6	49.6	49.6	49.6	49.6	49.6	49.6	50	50
1.8	1.8	1.9	1.9	1.9	2.0	2.0	2.1	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4	2.4
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US-09-032-337-44	US-09-560-639-5	PCT-US91-03478-1	US-08-442-043A-1	US-08-091-519-1	US-09-173-151A-15	US-09-173-151A-13	US-09-173-151A-5	US-09-227-717-3	US-07-821-716-3	PCT-US96-08899-3	PCT-US94-02414-3	US-08-466-932A-3	US-08-685-212-3	US-08-924-376-3	US-08-381-603-3	US-07-821-716-1	PCT-US96-08899-1
Sequence 44, F	Sequence 5, Ap	Sequence 1, Ap	Sequence 1, Ap	Sequence 1, Ap	Sequence 15, F	Sequence 13, P	Sequence 5, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 3, Ap	Sequence 1, Ap	Sequence 1, Ap
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## ALIGNMENTS

RESULT 1 US-08-991-944-1

Sequence 1, Application Patent No. 6280955

US/08991944

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US-08-991-944-1
                                                   Query Match
Best Local Similarity
Matches 1517; Conserv
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                                                                                                                                                                                                                                                                                              TELEFAX: (650) 343-4342 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
                                                                                                                                                                         MOLECULE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION TELEPHONE: (650) 343-4341
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/991,944 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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Nucleic Acids and Methods
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US-08-931-944-3
; Sequence 3, Application US/08991944
; Patent No. 6280955
; GENERAL INFORMATION:
APPLICANT: Cao, Zhaodan
: TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: PO-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER: US/08/991,944
FILING DATE:
CLASSIFICATION NUMBER: T97-014
REGISTRATION NUMBER: 36,627
REGISTRATION NUMBER: T97-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341

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; LOCATION:
US-08-991-944-3
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3355 base pairs
TYPR: nucleic acid
STRANDEDNESS: double
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 51.7%; Score 1067.4; Best Local Similarity 78.9%; Pred. No. 0; Matches 1298; Conservative 0; Mismatches
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              CGTACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCA
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                                                                                                                                                                     Sequence 3, Application US/09173151A Patent No. 6326472 GENERAL INFORMATION:
                                        APPLICANT: Timans, Jacqueline C.
APPLICANT: Debets, Johannes Eduard Ma
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Pr
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CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
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                                                            Proteins; Related Reagents and Methods
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Best Local Similarity 47.4%;
Matches 697; Conservative
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APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
PRIOR APPLICATION NUMBER: US 60/062,066
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APPLICATION NUMBER: US 60/078,008
APPLICATION NUMBER: 12-MAR-1998
APPLICATION NUMBER: 12-MAR-1998
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APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OFFWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
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                                                                                                                                         191 CTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGACCTTGAGGAGCCAATTA 250
                                                                                                                                                                                               149
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  263
                                           251 ACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCCGGCCCA 310
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CLASSIFICATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                      GCATTGACTGGTCAGTGGATCTCAAGACATACAT---GGCTTTGGCAGGTGAACCAGTCC 148
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                                                                                              CTGGGCTCAGGCTTATGTGGTACAAAAACA-----AAGGTGATTTGGAAGAGCCCATCA 262
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California
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Pred. No. 1.2e-38;
0; Mismatches 715; Indels 57; Gaps
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TIGAAGAAGAAGAGTTTGGTTTGAAGTACTGCCAGATGTCCTGGAAAAAACACTATGGAT 13	N i
11 AGTATGATATTTATGTATCCTATGCAAGGAATG 1243	1 12
10	Db 114
1 AGATGGTCCTATTTTACCGGGCTCATTTTGGAACAGATGAAACCATTTTAGATGGAAAAG 1	Qy 115
	Db 1082
_	Qy 109
22 ATGCCAGTGTTTTGCTGCGTAAAAAGGATTTAATCTATAAAATTGAGCTTGCAGGGGGCC 1081	Db 1022
	Qy 1031
68 AAGCTGACCTGGCGAATTATACCTGCCATGTTGAAAACCGAAATGGACGGAAAC 1021	vo
71 AGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCGAAGTTGCCAAAG 1030	Qy 97
8	Db 90
11 АТАБТАБААСАБААБАТБАААСААБААСТСАБАТТТТБАБСАТСААБАААБТТАССТСТБ 970	Qy 91
B AAGGAGAAAAGTTTATTGAAGAACTGGCAGGTCACATTAGAGAAGGTGAAATAAGGCTTC 907	Db 84
51 ТТGАПGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAAAGTATAAGTC 910	Ογ 85
88 TCCCCTGCAAAGCATTCTTCGGATTCAGTGGAGAGTCTGGGCCAATGATCTACTGGATGA 847	Db 78
	Оу 791
	Db 737
	Qy 731
77 CAACTGAATTGAAAGTTACAGCTTTACTCACAGACAAGCCTCCCCAAGCCATTGTTCCCCA 736	60
71 ATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCAGTGCCCCCTG 730	Ογ 67
17 AAGAAGATGGAGGAAATTACACATGTGAACTTAAATATGAAGGAAAACTTGTAAGACGAA 676	Db 61
11 TTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGACGTACGT	و <u>.</u> و
7 ANATGTGGAGAAGCATAATAATACAGAAAGGAAATGCTCTTCTGATCCAAGAAGTTCAAG .616	Db 557
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)7 ATGACTTTAAAAAGTCCGATCAGGAGCCTGATGTTGTGTGTG	Db · 49
-	· Qy 49
7 TCCCCTATTTAGAAAAATCTGAAGTCACTAAAAAGAAAGGAGATCTCCTGTCCAGACATGG 496	Db 437
	Oy 431
7 AGGTGTCAATGTCCTTGACTGTTGCAGAGAATGAATCAGGCCTGTGCTACAACAGCAGGA 436	Db 377
	Qy 371
CTGAGGCACAAGACAGTTGCATTCTACACTTGTGTTTTTAAGGAACTCAACATATTGCATGA	
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Patent No. 632647
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                                                                                                        TELEFAX: (650) 496-120
INFORMATION FOR SEQ ID NO:
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APPLICANT: I
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FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 1
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                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                  MOLECULE TYPE:
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PPLICANT: Kastelein, Robert A.
ITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
                                                                                                                                                     NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/0 FILING DATE: 14-OCT-1998
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                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
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                                                TOPOLOGY:
                                                          STRANDEDNESS:
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Debets,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         154 CACTTCTTGAAATTCAACTACAGCACAGCCCATTCAGCTGGCCTTACTCTGATCTGGTAT 213
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                                                                                                                                                                                                                                                                                                                                                 AGAACTCAGATTTTGAGCATCAAGAAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTC
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CGAGAGCTAATGTACACAGTGGAACTTGCTGGAGGCCTTGGTGCTATACTCTTGCTGCTT 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCACTATTGATGTCACCATTAACGAAAGTATAAGTCATAGTAGAACAGAAGATGAAACA 933
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                                                               APPLICATION DATA:
PRIOR APPLICATION UNIVERSE: US 60/081,883
APPLICATION NUMBER: US 60/081,883
APPLICATION NUMBER: 15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cent No.
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                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF IN
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APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
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                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/173,151A FILING DATE: 14-OCT-1998
                                         APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sana,
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Debets, Johannes Eduard Maria
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US 60/078,416
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Best Local Similarity
Matches 678; Conserv
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 15-OCT-
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                                                                                                                184 CATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGACCTTGAGGAG
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                                                                                                                                                                        124 CCAGCTCGCATCAAGTGCCCACTCTTGAACACTTCTTGAAATTCAACTACAGCACAGCC
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LOCATION:
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OTHER INFORMATION: /
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OTHER INFORMATION:
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LOCATION: 453..454
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REGISTRATION NUMBER:
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 342..343
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                                                      ccaattaactrececerececeaeaaceecartaetaaegagaaaagateteeteteete
                                                                                                                                              CCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTATAGCACGGCC
                                                                                    CAGAGCACTGGGCTCAGGCTTATGTGGTACAAAAACA----AAGGTGATTTGGAAGAG
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Pred. No. 6.3e-35;
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GAAGCAGTTTTTGATTTCAGTGAGAAGCAGAAGGATGATTGTTCTGAGCCCTGAC 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCAAAGCAGCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTGGCT 1083
                                                                                                                                                                                                                                       GGAAAAGAGTATGATATTTATGTATCCTATGCAAGG-------
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                                                                                                                                                                                                      AACAAGGAATATGATGCCTATCTCTTTACACAAAAGTGGACCAAGATACTTTAGACTGT
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Best Local 9
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APPLICANT: Parnet
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                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERRINCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELECHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1626 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1420 TATATTCTCAGACGGGGATGGAGTATTTTCGAACTGGAA 1458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 1200.
TELEFAX: 756822
                                                                               604 GCCTTAATTTCAAATAATGGAAATTACACATGTGTTACATATCCAGAAAAATGGACGT 663
583 CTATTTAATATCACCAAAAACCTTCAATATAACAATAGTGGAAGATCGCAGTAATATAGTT 642
                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
                                                                                                                                                                                                                                                                                                                                                CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                           ACGTTTCATCTCACCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCAGTG
                                                             GCCGAGTTTGAAGATCAGGGGTATTACTCCTGCGTGCATTTCCTTCATCATAATGGAAAA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATCTCACAAGATATGTTGAACAAAGCAGAAGACTTATTATCGTGCTAACTCCAGAC 1419
                                                                                                                        391;
                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
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51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1626 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                               CDS
1..1626
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1..57
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58..1623
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                                                                                                                         0;
                                                                                                                                      Score 89.6; DB 1;
Pred. No. 1.1e-18;
                                                                                                                        Mismatches
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                                                                                                                         429;
                                                                                                                                                     Length 1626;
                                                                                                                         Indels
                                                                                                                         24;
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Sequence 1, Application US/09110618 Patent No. 6090918
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOPTWARE: Microsoft Word, Version
                                                                                                                                                                                                                                                          APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAG
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51 University Street
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                                                                                                                                                                                                    Immunex Corporation
    5.1a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 4.3%;
Best Local Similarity 46.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: hu2F1
                                                            1024 GCCAAAGCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTGGCT 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              604 GCCTTAATTTCAAATAATGGAAATTTACACATGTGTTGTTACATATCCAGAAAATGGACGT 663
                                                                                                   883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGAGTTTGAAGATCAGGGGTATTACTCCTGCGTGCATTTCCTTCATCATAATGGAAAA 582
                        AGAAAAGCAGACATGGCTGATATCCCAGGCCACGTCTTCACAAGAGGAATGATCATAGCT
                                                                                                   TTATATAATTGCACTGTGGCCAGCACGGGAGGCACAGACACCAAAAAGCTTCATCTTGGTG
                                                                                                                                        ACCTCTGAGGATCTCAAGCGCAGCTATGTCTGTCATGCTAGAAGTGCCAAAGGCGAAGTT 1023
                                                                                                                                                                                AAATGGCATGCTTCAAAAGTATTGAGAATTGAAAATATTGGTGAAAGCAATCTAAATGTT
                                                                                                                                                                                                                   <u> АТАЛ GTC ATA GTA GAA CA GAA GAA CTCA GAA TTTTGA GCA TCA A GAA A GTT</u>
                                                                                                                                                                                                                                                              AATGGATCGGATCCTAATATACATGAAGAGAAAAGAAATGAGAATTATGACTCCAGAAGGC
                                                                                                                                                                                                                                                                                                  TGGACCATTGATGGAAAAAACCTGATGACATCACTATTGATGTCACCATTAACGAAAGT
                                                                                                                                                                                                                                                                                                                                         CTACTCATTCCCTGTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1626 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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58..1623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 89.6; DB 3;
Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
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1429 AGCA 1432

1354 GTCA 1357

US-09-110-618-1

GENERAL INFORMATION:
APPLICANT: Parnet

NUMBER OF SEQUENCES:

CORRESPONDENCE ADDRESS

ADDRESSEE:

STREET: 5.
STREET: 5.
STREET: 5.

COUNTRY:

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                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
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                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: Seattle
CITY: Seattle
WA
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            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                      TELEFAX: 1-1
                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
                                                     STRANDEDNESS:
                                                                                                                                                        TELEPHONE:
                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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51 University Street
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Best Local Similarity 46.3%;
Matches 391; Conservative
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NAME/KEY:
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TTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAG
                                TTATGCATATTTGAAAGGGATGTAGTGCCTGGAGGAGCTGTTGTTGATGAAATCCACTCA 1293
                                                          CTGTGCATCTTTGACCGAGACAGTCTGCCTGGGGGAAATACAGTGGAAGCAGTTTTTGAT
                                                                                                                       GGAAAAACATATGATGCTTTTGTGTCTTACCTAAAAGAATGCCGACCTGAAAATGGAGAG
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Pred. No. 1.1e-18;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 15-APR-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10-AUG-1
FILING DATE: 10-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING PRIOR DATA:
PRIOR APPLICATION DATA:
US 60/081,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                      NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 14-OCT
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                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/062,066 FILING DATE: 15-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60 FILING DATE: 12-MAR-1998
                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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Kastelein, Robert A.
VENTION: Human Receptor Proteins; Related Reagents and Methods
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Debets, Johannes Edua
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18-MAR-1998
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Score 88.6; DB 4;
Pred. No. 2.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                               FILING DATE: 22-DEC-1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 11
FILING DATE: 12-MAR-1:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                                          PRIOR APPLICATION DATA:
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                                                                          APPLICATION NUMBER: JP 215,488/1997 FILING DATE: 28-JUL-1997
                  APPLICATION NUMBER: FILING DATE: 09-OCT
                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLICANT: KURIMOTO, Musashi
TLE OF INVENTION: POLYPEPTIDES
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              имвек: JP 291,837/1997
09-ОСТ-1997
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NAME: BROWDY, Roger L REGISTRATION NUMBER:

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TELECOMMUNICATION INFORMATION:

202-628-5197

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SEQUENCE CHARACTERISTICS:
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Local Similarity 46.1%;
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TTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAG 1428
                                                                                                                                                               GGAAAAACATATGATGCTTTTGTGTCTTACCTAAAAGAATGCCGACCTGAAAATGGAGAG 1113
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                                         TTATGCATATTTGAAAGGGATGTAGTGCCTGGAGGAGCTGTTGTTGATGAAATCCACTCA 1233
                                                                              CTGTGCATCTTTGACCGAGACAGTCTGCCTGGGGGAAATACAGTGGAAGCAGTTTTTTGAT 1368
                                                                                                                          GAGCACACCTTTGCTGGAGATTTTTGCCCCAGGGTGTTGGAGAAACATTTTGGGTATAAG
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Pred. No. 5.5e-14;
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RESULT 11
US-08-996-338-7
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Query Match
Best Local Similarity 46.1
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Musashi
APPLICANT: KURIMOTO, MUSASHI
APPLICANT: FURIMOTO, POLYPEPTIDES
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FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291,837/1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PO NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1294 GTCA 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                           ORGANISM:
ORGANISM:
                                                                                           NAME/KEY: mat peptide LOCATION: 58..1620 IDENTIFICATION METHOD:
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OPERATING SYSTEM:
                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                             IDENTIFICATION METHOD:
                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patent In Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1620 base pairs
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                                                                                                                                                                                                                                                                                                                                       nucleic acid
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419 Seventh Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                       202-737-3528
                                                                                                                                                                                                                                        lymphoblastoid cell derived from a with Hodgkin's disease
                                                                                                                                                                             sig peptide
1..57
                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       202-628-5197
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IZ-MAR-1997
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               Score 75.2; DB 3;
Pred. No. 5.7e-14;
0; Mismatches 428;
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                  428;
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US-08-996-338-2
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                                                                                                                         Sequence 2, Application US/08996338 Patent No. 6087116
                                                                                                     GENERAL INFORMATION:
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APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Musashi
TITLE OP INVENTION: POLYPEPTIDES
NUMBER OP SEQUENCES: 37
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                                                                                                                                                                                                                                                                                                                                                               TTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGACAGAAAAG 1428
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                                                                                                                                                                                                                                                                                              AGCA 1432
                                                                                                                                                                                                                                                                                                                                     CTGATAGAGAAAAGCCGAAGACTAATCATTGTCCTAAGTAAAAGTTATATGTCTAATGAG
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Best Local Similarity
Matches 148; Conserv
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INFORMATION FOR SEQ ID NO:
                                1422
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REFERENCE/DOCKET NUMBER: TO TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 215,488/1997 FILING DATE: 28-JUL-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: JP 291,837/1997
1284
                                                                                                                                                                                                                                                                                                               1182 ААСАGATGAAACCATTTTAGATGGAAAAGAGTATGATATTTATGTATCCTATGCAAGGAA 1241
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patent In Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
                                                                                                                                                                                                                                                                                1044 AACAGATGGTAAAACATATGATGCCTTTGTGTCTTACCTGAAAGAGTGTCATCCTGAGAA 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
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STREET: 419 Sevent
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAMB/KEY: mat peptide LOCATION: 1..1557
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                                                                                                                                                           ATACAAGCTGTGCATCTTTGACCGAGACAGTCTGCCTGGGGGAAATACAGTGGAAGCAGT 1361
TAACGGAGCCAGGCGTGAGCTCGAGAGTGGACT
                                AGAMAAGAGCATCAGCATGCTGGAGTTTAMACT 1454
                                                                                           TTTTGATTTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGAC 1421
                                                                                                                                         GTATAAGTTATGCATATTTGAAAGAGATGTGGTGCCTGGCGGAGCTGTTGTCGAGGAGAT
                                                                                                                                                                                                           TAAAGAAGAGTATACTTTTTGCTGTGGAGACGTTACCCAGGGTCCTGGAGAAACAGTTTGG
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419 Seventh Street, N.W., Suite 300
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Pred. No. 2.9e-13;
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US-08-604-333-3; Sequence 3, Application US/08604333.; Patent No. 5776731; GENERAL INFORMATION:

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Best Local Similarity 54.2%;
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NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                             1598
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APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEMENT APPLICATION MINISTER STATEME
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLECULE TYPE:
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TELEPAX: 756822
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COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                                   CCATTCACTGATAGAGAAAAGCCGGAGGCTAATCATCGTTCTCAGCCAGAGTTACCTGAC 1717
                                                                                                                                                                                                  TTTTGATTTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGAC 1421
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                                                                   AGAAAAGAGCATCAGCATGCTGGAGTTTAAACT 1454
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51 University Street
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435..1991
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381..434
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US-09-110-618-3
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US-09-110-618-3
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 148; Conserv
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                                                         1538
                                                                             1478 AACAGATGGTAAAACATATGATGCCTTTGTGTCTTACCTGAAAGAGTGTCATCCTGAGAA 1537
                                                                                                                                            1182 AACAGATGAAACCATTTTAGATGGAAAAGAGTATGATATTTATGTATCCTATGCAAGGAA 1241
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 1598 GTATAAGTTATGCATATTTGAAAGAGATGTGGTGCCTGGCGGAGCTGTTGTCGAGGAGAT 1657
                         1302 ATACAAGCTGTGCATCTTTGACCGAGACAGTCTGCCTGGGGGAAATACAGTGGAAGCAGT 1361
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APPLICATION NUMBER:
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OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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LOCATION:
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REGISTRATION NUMBER: 32,172
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ilarity 54.2%;
Conservative
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Pred. No.
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RESULT 15
US-09-578-178-3
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Patent No. 6451760
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TELEX: 756822
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2830 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                  Query Match 3.5%;
Best Local Similarity 54.2%;
Matches 148; Conservative
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NAME/KEY:
LOCATION:
1182 AACAGATGAAACCATTTTAGATGGAAAAGAGTATGATATTTATGTATCCTATGCAAGGAA 1241
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NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,17
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft WO CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
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TITLE OF INVENTION: Receptor Designated 2F1
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cI
HYPOTHETICAL: NO
ANTI-SENSE: NO
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CLONE: mu2F1
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CITY: Seattle
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TELEFAX: (206) 233-0644
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                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                               NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                OCATION:
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Microsoft Word, Version 5.1a
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381..1994
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                                                Score 73; DB 4; Length 2830
Pred. No. 4.4e-13;
0; Mismatches 125; Indels
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                                                1422 AGAAAAGAGCATCAGCATGCTGGAGTTTAAACT 1454
                                                                                                    1658 CCATTCACTGATAGAGAAAAGCCCGGAGGCTAATCATCGTTCTCAGCCAGAGTTACCTGAC 1717
                                                                                                                                                       1362 TITTGATTTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGACTATGTGAC 1421
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Search completed: April 30, 2003, 09:41:32 Job time : 76 secs

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Minimum
Maximum
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*
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Listing first 45 summaries
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cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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9 US-10-011-548-34

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10 US-9-860-107-3616

10 US-9-864-761-4326

10 US-9-981-421-3

11 US-10-157-447-1

12 US-10-157-447-3

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US-09-864-761-16315
US-10-011-548-3
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US-10-215-211-5
US-09-935-868-27
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Sequence 34, Appli
Sequence 1, Appli
Sequence 3616, Ap
Sequence 4326, Ap
Sequence 3, Appli
Sequence 1, Appli
Sequence 235, App
Sequence 19, Appli
Sequence 3, Appli
Sequence 56, Appli
Sequence 7, Appli
Sequence 7, Appli
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Sequence 5, Appli
Sequence 27, Appl
Sequence 32830, A
Sequence 16315, A
Sequence 3, Appli
Sequence 21077, A
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1.9	1.9	1.9	1.9	1.9	1.9	1.9	2.0	2.0	2.0	2.1	2.4	2.4	2.4	2.4	2.6	2.7	2.7	2.7	2.8	2.9	2.9	2.9	2.9	2.9	2.9
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US-09-918-995-16653	US-10-184-634-332	US-10-184-644-332	US-09-921-667-7	US-09-854-162-1	US-10-199-209-1	US-10-215-211-1	US-10-011-548-15	US-10-212-287-1	US-10-011-548-13	US-10-011-548-5	US-09-775-046-14	US-09-731-175-3	US-09-880-107-2312	US-09-731-175-1	US-09-899-980A-4	US-09-899-980A-3	US-10-004-633-38	US-10-004-633-42	US-09-775-046-12	US-09-764-868-358	US-09-731-449-1	US-09-981-421-1	US-10-212-287-6	US-10-011-548-9	US-09-731-449-3
Sequence 16653, A	Sequence 332, App	Sequence 332, App	Sequence 7, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 15, Appl	Sequence 1, Appli	Sequence 13, Appl	Sequence 5, Appli	Sequence 14, Appl	Sequence 3, Appli	Sequence 2312, Ap	Sequence 1, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 38, Appl	Sequence 42, Appl	Sequence 12, Appl	Sequence 358, App	Sequence 1, Appli	Sequence 1, Appli	Sequence 6, Appli	Sequence 9, Appli	Sequence 3, Appli

## ALIGNMENTS

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US-10-215-211-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1713
                                                                                                                                                                                                                                          Query Match 67.1%;
Best Local Similarity 89.4%;
Matches 1515; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/215,211
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sims, John E.
APPLICANT: Smith, Dirk E.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS
FILE REFERENCE: 3321-A
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)..
                                  121
181 GCCCATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGACCTTGAG
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; SEQ ID NO 5; LENGTH: 1077; TYPE: DNA ORGANISM: Homo sapiens FEATURE: CDS LOCATION: (1)..(1077); CTHER IMPORMATION: US-10-215-211-5
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Publication No. US20030049255A1
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Simth, Dirk B.
APPLICANT: Smith, Dirk B.
TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN THE TREATMENT OF DISEASES
FILE REFERENCE: 3321-A
CURRENT APPLICATION NUMBER: US/10/215,211
CURRENT FILING DATE: 2002-08-07
PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOPTWARE: PatentIn version 3.1
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RESULT 3
US-09-935-86B-27
Sequence 27, Application US/09935868
Patent No. US20020164690A1
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Receptor Based Antagonists, any FILE REFERENCE: REG 203D
CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
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Pred. No. 1.7e-314;
0; Mismatches 3;
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                                                           SEQ ID NO 32830
LENGTH: 287
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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                                                                                                                                             NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/180,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: Aeomica-X-1
                                      FEATURE:
    OTHER INFORMATION: OTHER INFORMATION:
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FILLING DATE: 2000-08-03
APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00667 FILING DATE: 2001-01-30
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                                                                                                                                                                                                             APPLICATION
                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                       FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/234,687
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00670
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APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/236,359
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NUMBER: PCT/US01/00668
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MAP TO AC008249.14
EXPRESSED IN HELA, SIGNAL
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                                                                                                                                                                                                         US 09/774,203
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US-09-864-761-16315

Sequence 16315, Applicatio Patent No. US20020048763A1

Application US/09864761

APPLICANT: Penn, Sharron

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INFORMATION:
INFORMATION:
INFORMATION:
              GGCCCACTCTCCATGACGCCCCCTATACCTGCATGTTAAGG
                                                        CAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCC
                                                                                                                                                                      CAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGCCC
                                                                                                                                                                                    CAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGGCC
                                                                                                                                                                                                                                                      AACGCTGCGATGACTGGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTTGAAGATGAGC
GGCCCACTCTCCAATGACACTGGCAACTATACCTGCATGTTAAGG
                                                                       CAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCC
                                                                                                               ATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGACCTTGAGGAGC
                                                                                                                               ATTCAGCTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGGACCTTGAGGAGC
                                                                                                                                                                                                                                                                                   287;
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                        EXPRESSED IN PLACENTA, SIGNAL = 1.8
EST HUMAN HIT: BE892231.1, EVALUE 0.00e+00
NT HIT: AP167336.1, EVALUE 0.00e+00
SWISSPROT HIT: Q02955, EVALUE 7.00e-03
                                                                                                                                                                                                                                                                                                 13.9%;
                                                                                                                                                                                                                                                                                                 Score 287;
Pred. No.
                                                                                                                                                                                                                                                                                     Mismatches
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APPLICANT: Hanzk, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL PO)
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT PELICATION NUMBER: US 60/180,312
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PELILING DATE: 2000-05-26
PRIOR PELILING DATE: 2000-05-26
PRIOR PELILING DATE: 2000-05-26
PRIOR PELILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR PELICATION NUMBER: US 60/236,359
PRIOR PELILING DATE: 2000-01-0-04
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PELILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELILING DATE: 2001-01-30
PRIOR PELILIN

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US-10-011-548-3
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Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacquelin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 220;
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SOFTWARE: Annomax Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/00670 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: US 60/234,687 PRIOR FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO AC008249.14 OTHER INFORMATION: EXPRESSED IN HELA, OTHER INFORMATION: EXPRESSED IN PLACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439
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                                               ZIP: 94304-1104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62
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                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Human Receptor Proteins; Related Reagents Methods
                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATG
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                                                                                                                                                                                                                             CITY: Palo Alto
STATE: California
COUNTRY: USA
                     CLASSIFICATION: <Unknown>

   APPLICATION DATA:
APPLICATION NUMBER: 09/173,151
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Debets, Johannes Eduard Maria
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Bazan, J. Fernando
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100.0%; Pr
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131
                                     491
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                                                                                                                                                                                             371 AAGTTGCATTTCCCTTGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCCCCCCATGAAAC 430
                                                                                                                                                                                                                                       317
                                                                                                                                                                                                                                                                            311 CTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACATATTGCAGCA 370
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FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 1..2058
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGCCCATTCAG 190
                                                                                                     TCCCAGTGCATAAACTGTATATAGAATATGGCATTCAGAGGATCACTTGTCCAAATGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGCCTTACTCTGATCTGGTATTGGACTAGGCAGGACCGGGACCTTGAGGAGCCAATTA 250
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ATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGCTGTTATAAAA 550
                                                                            TCCGCTATTTAGAAAATCTGAAGTCACTAAAAGAAAGGAGATCTCCTGTCCAGACATGG
                                                                                                                                                          AGGIGTCAAIGTCCTTGACTGTTGCAGAGAATGAATCAGGCCTGTGCTACAACAGCAGGA 436
                                                                                                                                                                                                                                                                                                                                                                                                  CTGGGCTCAGGCTTATGTGGTACAAAAACA----AAGGTGATTTGGAAGAGCCCCATCA
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: <Unknown>
APPLICATION NUMBER: US 6
FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/095,987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 12-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICATION NUMBER: US 60/081,883
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Pred. No. 6.7e-35;
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                                                                                                   RESULT 7
US-09-864-761-21077
             GENERAL INFORMATION:
APPLICANT: Penn, Shi
APPLICANT: Rank, D.
                                                                  Sequence 21077, Application Patent No. US20020048763A1
   APPLICANT:
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                                                                                                                                                                  GACGGGGATGGAGTATTTTCGAACTGGAA
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PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 2001-01-30
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                                                                                                                                                                                     NN: MAP TO AC008249.14

NN: EXPRESSED IN BT474, SIGNAL = 1.3

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6

NN: EXPRESSED IN HELA, SIGNAL = 1.2

NN: EXPRESSED IN HELA, SIGNAL = 1.7

NN: EXPRESSED IN PLACENTA, SIGNAL = 1.7

NN: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

NN: EXPRESSED IN BRAIN, SIGNAL = 1.3

NN: EXPRESSED IN HEAT, SIGNAL = 1.2

NN: EXPRESSED IN HEAT, SIGNAL = 1.6

NN: EXPRESSED IN HELLOO, S
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Score 149; DB IV,
Pred. No. 4.9e-35;
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                                                                  Length
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US-10-011-548-34
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Publication No. US20030055218A1
GENERAL INFORMATION:
                                                                                                                                                INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 2537 base pairs
TYPE: nucleic acid
STRANDENNESS: single
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FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                NAME/KEY: CDS
LOCATION: 1..2004
SEQUENCE DESCRIPTION: SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                       FEATURE:
                                                                                                            MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
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                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                         TELEPAX: (650)496-1200
                                                                                                                                                                                                                                                                                              TELEPHONE: (650)852-9196
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Kastelein, Robert A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      574 CCCGAAGGTATGAACTTGAGTTTCCTCATTGCCTTAATTTCAAATAATGGAAATTACACA 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                442 GAACCTGAAATCCTTTGGTACAAGGAATGCAGGACAAAAACATGGAGGCCAAGTATTGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 ATGAGGCAAATCCAAGTGTTTGAAGATGAGCCAGCTCGCATCAAGTGCCCACCTCTTTGAA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                       CCAGCTCCAAGATACACAGTGGAACTGGCTTGTGGTTTTTGGAGCCACAGTCCTGCTAGTG 1113
                                                                                                                                                               GAACAGGAAGTTTCCATCTCATTAATTGTGGACTCTGTGGAAGAAGGTGACTTGGGAAAT 909
                                                                                                                                                                                                      AGAACTCAGATTTTGAGCATCAAGAAAGTTACCTCTGAGGATCTCAAGCGCAGCTATGTC
                                                                                                                                                                                                                                                                                     ATCACTATTGATGTCACCATTAACGAAAGTATAAGTCATAGTAGAACAGAAGATGAAACA 933
                                                                                                                                                                                                                                                                                                                                                                                                              AAGGTAGTAGGCTCTCCAAAAAATGCAGTGCCCCTGTGATCCATTCACCTAATGATCAT 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTCAAAAAGACAGCTGTTTCAATTCCCCCATGAAACTCCCAGTGCATAAACTGTATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGACTAGGCAGGACCGGGACCTTGAGGAGCCAATTAACTTCCGCCTCCCCGAGAACCGC 273
CGAGAGCTAATGTACACAGTGGAACTTGCTGGAGGCCTTGGTGCTATACTCTTGCTGCTT 1029
                                                                                                                                                                                                                                            GATCTGGATGAAAATCGAGTTTGGGAAAGTGACATTAGAATTCTTAAGGAGCATCTTGG
                                                                                                                                                                                                                                                                                                                                                                    TTTCTGATGGATTCTCGCAATGAGGTTTGGTGGACCATTGATGGAAAAAAACCTGATGAC 873
                                                                            TACTCCTGTTATGTTGAAAATGGAAATGGACGTCGACACGCCAGCGTTCTCCTTCATAAA 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTGTTACAGCCCCTCTGACTGATAAGCCACCCAAGCTTTTGTATCCTATGGAAAGTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATACCTGCATGTTAAGGAACACTACATATTGCAGCAAAGTTGCATTTCCCCTTGGAAGTT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTAGTAAGGAGAAAAGATGTGCTGTGGTTCCGGCCCACTCTCCTCAATGACACTGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTATATCÁGAACAAATTACTCCCTTGCCCAAAGTGCTGGACTCAGTTTGATGTGGTAC 147
                                                                                                                     TGTCATGCTAGAAGTGCCAAAGGCGAAGTTGCCAAAGCAGCCAAGGTGAAGCAGAAAGTG
                                                                                                                                                                                                                                                                                                                         GGGTACAGCGGAGATGTCAGTCCTTTAATTTACTGGATGAAAGGAGAAAAATTTATTGAA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTGTTGTTACATATCCAGAAAATGGACGTACGTTTCATCTCACCAGGACTCTGACTGTA 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGCCTGTGTCATCAGGAACTCCACTTACTGTATGAAAGTATCCATCTCACTGACAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 7.9e-33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10011548 Publication No. US20030055218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1210 GAAATCCTACCTGATATGCTTGAAAAAGCATTATGGATATAAGTTGTTTATACCAGATAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1150 ACCAAAGTGGATCCTGACCAGTGGAATCAAGAGACTGGGGAAGAAGAACGTTTTGCCCTT 1209
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible operATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGACCCTCCGTGGAGTTTTGGAGAATGAATTTTGGATACAAGCTGTGCATCTTTGACCGA 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTAAA 1452
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                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                    APPLICATION NUMBER: 09/173,151
FILING DATE: "Unknown"
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/011,548 FILING DATE: 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Palo Alto
STATE: California
                                           APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998
                                                                                                                                      APPLICATION NUMBER: US 60/078,008 FILING DATE: 12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
APPLICATION NUMBER: US 60/078;416 FILING DATE: 18-MAR-1998
                                                                                       APPLICATION NUMBER: US 60/081,883 FILING DATE: 15-APR-1998
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Debets, Johannes Edua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            901 California
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                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.8
Matches 678; Conservative
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SEQUENCE CHARACTERISTICS:
                                                             244
                               241
                                                                                             187
                                                                                                                    184 CATTCAGCTGGCCTTACTCTGATCTGGATTGGACTAGGCAGGACCGGGACCTTGAGGAG 243
                                                                                                                                                           127
                                                                                                                                                                                       124 CCAGCTCGCATCAAGTGCCCACTCTTTGAACACTTCTTGAAATTCAACTACAGCACAGCC 183
304 CGGCCCACTCTCCTCAATGACACTGGCAACTATACCTGCATGTTAAGGAACACTACATAT 363
                                                                                                                                                                                                                        64 GAACGCTGCGATGACTGGGGACTAGACACCATGAGGCAAATCCAAGTGTTTGAAGATGAG 123
                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "splice junction" SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 15-OCT-19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                            CCAATTAACTTCCGCCTCCCCGAGAACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTC 303
                                                                                                                                                            CCAGTCCGAGTGAAATGTGCCCTTTTCTACAGTTATATTCGTACCAACTATAGCACGGCC 186
                                                                                             CAGAGCACTGGGCTCAGGCTTATGTGGTACAAAAACA----AAGGTGATTTGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
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OTHER INFORMATION: /not
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OTHER INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
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GAAGATCTCACAAGATATGTTGAACAAAGCAGAAGACTTATTATCGTGCTAACTCCAGAC 1419
                                          GAAGCAGTTTTTGATTTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTGAGCCCTGAC 1413
                                                                                                                                                                                                                                                                      AACAAGGAATATGATGCCTATCTCTCTTACACAAAAGTGGACCAAGATACTTTAGACTGT 1239
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APPLICATION NUMBER: GB 24263.6

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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
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                                                                                                                                                                                                                                                                                                                                               Sequence 4326, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
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Best Local
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                       TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
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LOCATION: (1)..(443)
OTHER INFORMATION: n = a or c or g or
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ORGANISM: Homo sapiens
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Local Similarity 89.4%;
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                                                                                                                                                                                                                                   Rank, David R.
Hanzel, David K.
Chen, Wensheng
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Sest Local Similarity
Watches 95; Conserv
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                                                                                                              Sequence 3, Application US/09981421 Patent No. US20020098185A1
                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 4326
           APPLICANT: Sims, John E.
APPLICANT: Wohler, Kendall M.
APPLICANT: Born, Teresa L.
TITLE OF INVENTION: METHODS FO
FILE REFERENCE: 3086-A
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APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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EXPRESSED IN BT474, SIGNAL = 1.3
EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
EXPRESSED IN BONE MARROW, SIGNAL = 1.2
EXPRESSED IN HELA, SIGNAL = 1.8
NUMBER: US/09/981,421
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Pred. No.
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N ADULT LIVER, SIGNAL = 1.3

N BRAIN, SIGNAL = 1.3

N LING, SIGNAL = 1.2

N HEART, SIGNAL = 1.6
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PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
SOPTWARE: PatentIn version 3.1
SEQ ID NO 3
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)
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                                                                                                                                 GGAAAAGAGTATGATATTTATGTATCCTATGCAA------GGAATGCGGAA 1248
                                                                                                                                                                                                                                                       TGGCTAGAGATGGTCCTATTTTACCGGGCTCATTTTGGAACAGATGAAACCATTTTAGAT
                                                                                                                                                                                                                                                                                                                                 TGTGGTTTTGGAGCCACAGTCCTGCTAGTGGTGATTCTCATTGTTTTTACCATGTTTAC 1143
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                                                                    CTGTGCATCTTTGACCGAGACAGTCTGCCTGGGGGAAATACAGTGGAAGCAGTTTTTGAT
                                                                                                             GAGCACACCTTTGCTGTGGAGATTTTTGCCCCAGGGTGTTGGAGAAACATTTTGGGTATAAG
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Pred. No. 2.9e-16;
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US-10-157-447-1
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Matches 391
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INFORMATION FOR SEQ ID NO: 1:
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604 GCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGACGT 663
                                                             Local Similarity
les 391; Conser
                                                                                                                                                           SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
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TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Receptor Designated
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                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
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                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
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CLASSIFICATION: <Unknown>
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OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, V
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FILING DATE: «Unknown».
APPLICATION NUMBER: 09/110,618
FILING DATE: «Unknown»
                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                     CLONE: hu2F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/10/157,447
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Conservative
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MBER: 32,172
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                                                           Score 89.6; DB 12;
Pred. No. 2.9e-16;
0; Mismatches 429;
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Street
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                                                                                                                                                                         Sequence 235, Application US/09764853 Patent No. US20020090672A1 GENERAL INFORMATION:
   SEQ ID NO 235
         APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZO6
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
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US-09-764-853-235
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Best Local Similarity 52.8
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19, Application US/10011548
Publication No. US20030055218A1
GENERAL INFORMATION:
APPLICANT: Timans, Jacqueline
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           COMPUTER READABLE FORM:

"MEDIUM TYPE: Ploppy disk
"MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible.
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                   Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA
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                                                                                                                                                                                                                             STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                                           ZIP: 94304-1104
                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                            STATE: California
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Debets, Johannes Eduard Maria
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Pred. No. 6.7e-16;
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                                                                                                                                                                                                                                                                                                                                       Proteins; Related Reagents
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                                                                                     Version
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-10-011-548-19
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Best Local Similarity
Matches 236; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1033 GCCAAGGTGAAGCAGAAAGTGCCAGCTCCAAGATACACAGTGGAACTGGCTTGTGGTTTT 1092
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823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                GATTTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCTTGAGCCCCTGACTATGTGACAGAA 1425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCAGCGTTCTCCTTCATAAACGAGAGCTAATGTACACAGTGGAACTTGCTGGAGGCCTT
                                AAGAGCATCAGCATGCTGGAGTTTAAA 1452
                                                                                AGATGTGTAGATCAAAGCAAGCGGCTGATTATTGTCATGACCCCAAATTACGTAGTTAGA
                                                                                                                                                                                                       ААССТСТСКАТСТТТСАСССАСАСАСТСТСССТССССБАААТАСАСТССАААССАСТТТТ 1365
                                                                                                                                                                                                                                                  GAAGAAGAACGITTTGCCCCTTGAAATCCTACCTGATATGCTTGAAAAGCATTATGGATAT 702
                                                                                                                                                                                                                                                                                                                                   TATGATGCATACTTATCATACACCAAAGTGGATCCTGACCAGTGGAATCAAGAGACTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                   ATCATGCTCTTCTACAGGAATCATTTTGGAGCTGAAGAGCTCGATGGAGACAATAAAGAT 582
                                                                                                                                                                  LENGTH: 1991 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 34,090 REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998 APPLICATION NUMBER: US 60/078,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/078,008 FILING DATE: 12-MAR-1998 APPLICATION NUMBER: US 60/081,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/065,776 FILING DATE: 17-NOV-1997 . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 09/173,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 18-MAR-1998
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Pred. No. 6.7e-16;
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Search completed: April 30, 2003, 10:47:51 Job time: 184 secs

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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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2064
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16722.103 Million cell updates/sec
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24.9	5 601.2 29.1 880 13 BI330085	30.6 814 14	34.0	34.3 849 9	50.3 1549	Result Query No. Score Match Length DB ID	
AL544533		4 BQ006059	3 BI862501	AL543511	1 BC016141	ID	
AL544533 AL544533	BI330085 60298218	BQ006059 UI-H-EI1	BI862501 60339062	AL543511 AL543511	Ø	Description	

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## ALIGNMENTS

	REMARK	JOURNAL	RBFBRENCE AUTHORS	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 BC016141 LOCUS DEFINITION
Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC/DCTD/DTP CDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,	USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk	Direct Submission .  Submitted (22-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1549) Strausberg,R. Strausberg,R.	TMAGE: 3920152, mRNA. BC016141.1 GI:16359373 HTC. HTC. Homo sapiens. Homo sapiens	BC016141 1549 bp mRNA linear HTC 24-OCT-2001 Homo sapiens, interleukin 1 receptor accessory protein, clone

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BASE COUNT
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ATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTGTACATATCCAGAAAATGGA
                                                                                    TGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTC
                                                                                                                                                                        CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC
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                                                                TGTTATAAAATACAGAATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTC
                                                                                                                                                CCAAATGTAGATGGATATTTTCCTTCCAGTGTCAAACCGACTATCACTTGGTATATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 15 Row: 1 Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4504660 This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480
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/clone_Tib="NIH' MGC 72"
/lab_host="DH10B" _____
/note="Vector: pCMV-SPORT6"
340 c 331 g 398 t
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/db_xref="LocusID:3556"
/db_xref="taxon:9606"
/clone="IMAGE:3920152"
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Pred. No. 1.6e-297;
0; Mismatches 0;
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Query Match Best Local Similarity

34.3%; 99.4%;

Score Pred.

708.6; DB 9; No. 3e-199;

Length 849

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JOURNAL COMMENT
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
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1 (bases 1 to 849)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
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                232
         /organism="Homo sapiens"
/db xref="taxon:9606"
/clone="CSOD1003YK15"
/clone lib="LTI NFL006 FL2"
/tissue type="placenta"
/note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA
/mas primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
2 others
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                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 873)
                                                                                                                                                                                 mRNA sequence.
BI862501
                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                     Homo sapiens
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§03390624F1 NIH_MGC_87 Homo sapiens
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Incyte Genomics, Inc.
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                                                                       GACATCACTATGTGATGTCACCATTAACGAAAGTATAAGTCATAGTAGAACAGAAGATGA
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Pred. No. 3.8e-197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov The following repetitive elements were found in this CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
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BQ006059.1 GI:19730959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg,
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                                                                                                                                                                                        206
                                                                       Conservative
                                                                                                                                                                                                                                                                                          /lab_host="DHIOB (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
with a modified polylinker; Site 1: ECOR I; Site 2: Not I;
NCI CGAP EII is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma. The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I Site. Double stranded cDNA was ligated to an ECOR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                      TAG_LIB=UI-H-EI1
TAG_TISSUE=chondrosarcoma
TAG_SEQ=ACACTTGCAC"
164 c 157 g 286
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tissue_type="Chondrosarcoma"
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                                                                                           30.6%;
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                                                                   Score 632.2; DB 14
Pred. No. 1.7e-176;
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                                BI330085 880 bp mRNA linear EST 30-JUL-2001 602982187F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5135061 5',
 BI330085.1
            mRNA sequence.
BI330085
  GI:15014755
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LOCUS
DEFINITION
DEFINITION
6029921871 NCI CGAP Li9 Mus musculus cDNA clone IMAGE:5135061 5'
ACCESSION
ACCESSION
EST.
BI330085.1 GI:15014755
SOURCE
ONGANISM
Mus musculus
Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
REFERENCE
1 (bases 1 to 880)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Tissue Procurement: Jeffrey E. Green, M.D.
CONTALI: capabs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11331 row: n column: 22
High quality sequence stop: 870.
FEATURES

BI330085

BRNA clone IMAGE: SINC (INAGE: SINC)

BI330085.1 GI:15014755

BRAGE: SINC (INAGE: Consortium/LLNL)

BRAGE: SINC (INAGE: LLAM11331 row: n column: 22

High quality sequence stop: 870.

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TTCACCGGAAAGATGAAACCAGGACTCAGAATTTGAGCATCAAGAAAGTCACCCCGGAGG
                                                                             GAAAAAAACCTGATGACATCACTATTG-ATGTCACCATTAACGAAAGTATAAGTCATAGT
                                                                                                                                              GTACGGTCTATTTTAGTTTTCTGATGGATTCTCGCAATGAGGTTTGGTGGACCATTGATG
                                                                                                                                                                                                                                                                      CCAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCAGTGCCCCCCTGTGATCC 736
                                                                                                                                                                                                                                                                                                                                     ATTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTCATTGCCTTAATTTCAA 616
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                                                           GAPAGAAGCCTGATGACGTCACAGTCGAACATCACTATTAATGAAAGTGTAAGTTATTCT
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/clone_lib="NCI_CGAP_Li9"
/clone_lib="NCI_CGAP_Li9"
/lab_host="DHIOB (Tl_phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: Cloned unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/strain="FVB/N"
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                                                                                                                                  CTGGCAACTATACCTGCATGTTAAGGAACACTACATATTGCAGCAAAGTTGCATTTCCCT 385
                                                                                                                                                                                                                    AACCGCATTAGTAAGGAGAAAGATGTGCTGTGGTTCCG--GCCCACTCTCCTCAATGACA 325
                                                                                                                                                                                                                                                                      TGGTATTGGASTAGGGRGGGGGGGGGGTTGAGGAGGGAATTAAGTTGGGGTGGGGGAG
                                                                                                                                                                                                                                                                                                                                                          TITGAACACTICTIGAAATICAACIACAGCACAGCCCATICAGCIGGCCTIACTCIGAIC 207
TGTATATAGAATATGGCATTCAGAGGATCACTTGTCCAAATGTAGATGGATATTTTCCTT
                 TGTATATAGAATATGGCATTCAGAGGATCACTTGTCCAAATGTAGATGGATATTTTCCTT 505
                                                               TGGAAGTKGTTSAAAAAGACAGSTGTTTGAATTCSCCCATGARACTCCCAGTGCATAAAC 593
                                                                               TGGAAGTTGTTCAAAAAGACAGCTGTTTCAATTCCCCCATGAAACTCCCCAGTGCATAAAC 445
                                                                                                                                                                                                      AAGGGSATTAGIRRGGRGRARGAIGIGGKGIGGTIGGGGSGCGCASISISSISAAIGACA 473
                                                                                                                                                                                                                                                                                                       TGGTATTGGACTAGGCAGGACCGGGACCTTGAGGAGCCAATTAACTTCCGCCTCCCCGAG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: PCWVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the NotI and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fullength.invitrogen.com"

http://fulllength.invitrogen.com"

218 t 57 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
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/db_xref="taxon:9606"
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1 (bases 1 to 596)

Xu,X.; Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Pu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Chen,Z. and Han,Z.

Hu,G., Gu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,

Hu,G., Gu,J., Hu,W., M., Mu,J., Hu,W.,

Hu,G., Gu,J., Hu,M., Mu,J., Hu,W.,

Hu,G., Gu,J., Hu,M., Mu,J., Hu,W.,

Hu,G., Gu,J., Hu,M., Mu,J., Hu,M.,

Hu,G., Gu,J., Hu,M., Mu,J., Hu,M.,

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Hu,G., 
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 1
201203, P. R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 86-21-50801919(ex.45)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hanzg@chgc.sh.cn
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/db_xref="taxon:9606"
/clone="GLCEPH02"
                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="GLC"
/tlssue_type="corresponding non cancerous liver
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                          note="Vector: pBluescript sk(-);
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 789)
                                                                                                                                                                                       Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
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                                                                                                                                                                               Fax: 86-21-50801922
                                                                                                                                                                                                                                                                      21625106
                                                                                                                                l: hanzg@chgc.sh.cn
clone is available at CHGC
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLC Homo sapiens
             /tissue_type="corresponding
/dev_stage="Adult"
/lab_host="SOLR"
                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCFUB08"
                                                         clone_lib="GLC"
   note="Vector:
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pBluescript sk(-); Site_1:
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Best Local Similarity
Matches 512; Conserv
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                                                                                                                                                                                                            AUTHORS
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., To, Lacy,M., Le,M., Walter, C., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                               AI303998 756 bp .mRNA linear EST 08. ui63d12.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1887095 5' similar to gb:X85999 M.musculus mRNA for interleukin 1 receptor accessory (MOUSE);, mRNA sequence.
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                Mus musculus
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CTTTTCATATGTACTACNCNGAGGCATGAACTTNGAGCTNTTCATTCNCTTGGTTTCATA
                                TTTTAATAATGTAATACCCGAAGGTATGAACTTGAGTTTCCTCATTGCCTTAATTTCAAA
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ilarity 82.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: liver; Vector: pME18S-FL3; Site_1: DraIII (CACCTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligic(aT) primer [ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was proported to the part of the cDNA insert.
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/lab_host="DH10B"
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	Oy 744 TAATGATC	Qy 684 TCTGACTG	Qy 624 AAATTACA         Db 1 AAATTACA	Query Match Best Local Similarity Matches 596; Conser	BASE COUNT 206 ORIGIN	; ;	South	MGI:1 Seq I High	Emall: Tissue cDNA; cDNA; DNA S Clone found	JOURNAL Unpubli	TITLE Nation	2	VERSION AW211290.1 KEYWORDS EST. SOURCE house mouse		RESULT 10 AW211290 LOCUS DEFINITION u079b07.	Qy 678 CAGGACTC             Db 662 CANGACTG	Qy 618 TAATGGAA           Db 602 ATACGGCA
or 5.5. on 5.5. on 5.5. on 5.5. on 5.5. on 6.5. on 6.5	TAATGATCATGTGGTCTATGAGAAAGAACCAGGAGAGGAGCTACTCATTCCCTGTACGGT 803	TCTGACTGTAAAGGTAGTAGGCTCTCCAAAAAATGCAGTGCCCCCTGTGATCCATTCACC 743 	AAATTACACATGTGTTACTTACATATCCAGAAAATGGACGTACGT	24.2%; Score 499.6; DB 10; Length 72 82.4%; Pred. No. 5.3e-137; vative 0; Mismatches 125; Indels	22, 37-43 (1999)." a 148 c 182 g 186 t 1	pe="tumor, gross tissue"  ="10 months"  ="10 months"   phiobs   pin: mammary; Vector: pCMV-SPORT6; Site 1: sit; Cloned unidirectionally. Primer: Oligonstructed by Life Technologies. Investigate samples: Lothar Hennighausen/Chu-Xia Deng, for transgenic model: Xu et al., Nature Ger	Janism="Mus musculus" Janism="129,C57BL/6J,FVB/) xxref="taxon:10090" nne="IMACB:2648725" one_lib="NCI_CGAP_Mam3"	-40RP from Gibc y sequence stop: cation/Qualifier	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can b found through the I.M.A.G.E. Consortium/LLNL at: "www-bio.llnl.gov/bbrp/image/image.html	t: Robert Strausberg,	//www.ncbi.nlm.nih.gov/ncicgap. //www.ncbi.nlm.nih.gov/ncicgap.	120a; Chordata; Craniata; Vertebrata; Euteleosto 121a; Rodentia; Sciurognathi; Muridae; Murinae;	. 0	ur to gb:X85999 M.musculus mRNA for interleukin 1 receptor oory (MOUSE);, mRNA sequence. 90	90 723 bp mRNA linear EST 03-DEC-1999 77.y1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:2648725 5'	CAGGACTCTGACTGTAAAGGTAGTAGGCTCTCCAA 712	TAATGGAAATTACACATGTGTTGTTACATATCCAGAAAATGGACGTACGT

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REFERENCE
AUTHORS
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                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 910)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                910 bp mRNA linear EST 20-OCT-2 mRNA sequence. MRNA sequence. MRNA sequence. MRNA sequence.
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9751 row: a column: 17
High quality sequence stop: 710.
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Location/Qualifiers 1. .910 /organism="Homo sapiens"

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RESULT 12
BM760155
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Best Local Similarity 93.8%;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     5', mRNA sequence.
BM760155
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                                                                                                                                                                           K-EST0040658 S2SNU668s1 Homo sapiens cDNA clone S2SNU668s1-14-A03
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/clone="IMAGE:3920152"
/clone_ib="NIH_MGC_72"
/clone_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo of Average insert size 2 kb. Library constructed by Life Technologies."
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                                                                                           ACTTGAGTTTCCTCATTGCCTTAATTTCAAATAATGGAAATTACACATGTGTTGTTACAT
                                                                                                                 ACTIGAGTITICCTCATTGCCCTTAATTTCAAATAATGGAAATTACACACATGTGTTGTTACAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Korea Research Institute of Bioscience & Biotechnology 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 489.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: yongsung@mail.kribb.re.kr
Plate: 14 row: A column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: +82-42-860-4409
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ilarity 100.0%;
Conservative
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Site 2: NotI; The poly (A)+ RNA was decapped with tabacco
acid pyrophosphatase (TAP) and ligated with DNA-RNA linker
including EcoRI site by treatment of T4 RNA ligase. The
first strand cDNA was synthesized from oligo dT-selected
mRNA by priming with dT-tailed vector. The dT-tailed
vector was adjusted to have about 60nt. The cDNA vector
was circularized with E. coli DNA ligase after digestion
of EcoRI which site is also included in vector. An RNA
strand converted to a DNA strand by Okayama-Berg method.
The obtained cDNA vectors were used for transformation of
competent cells E. coli TOP10F' by electroporation of
colonies in original cDNA library, the abundant cDNAs were
selected and amplified by PCR reaction using vector region
primer including T7 promotor as 5' primer and N(dT)14 as
3' primer. The PCR products were used as template for
synthesis of biotinylated single stranded RNA by in vitro
transcription reaction. The synthesized RNA probes were
hybridized with antisense single stranded cDNAs prepared
from original liberary and incubated with avidin-gel.
After removing DNA-RNA hybrids by centringe, the
subtracted cDNA libraries were constructed by
transformation of the remaining DNA into competent cells E.
coli Top10F' with electroporation method."

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/db_xref="taxon:9606"
/clone="$2$NU668$1-14-A03"
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/cell_line="SNU-668"
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AGATGAAACAAGAACTCAGATTTTGAGCATCAAGAAAGTTACCTCTGAGGATCTCAAGCG 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCACCATTAACGAAAGTATAAGTCATAGTAGAACAGAAGATGAAACAACAACAACTCAGATTT 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCGCAATGAGGTTTGGTGGACCATTGATGGAAAAAAACCTGATGACATCACTATTGATG
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                                                                                                                                                                                                                                                                                Seq
                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with
v0.980904.e. Vector identified by cross_match with the -mi
                                                                                                                                                                                                                                                                                                                                                                                                                                  PO Bo
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376288 MARC 2PIG Sus sc:
BI346913
BI346913.1 GI:15040211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pig.
Sus scrofa
                                                                                                                                                                                                                                                                                Plate: 130 row: L column: 3
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST discovery in swine 
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 580)
Fahrenkrug, S.C., Fr
                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
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Box 166, Clay Center, N
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402 762 4390
                                               Conservative
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                                                                                                                                                                           /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC_2PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                    /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 110 c 158 g 153 t
                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                             23.6%;
91.8%;
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                                               0,
                                            Score 486.4; DB 13;
Pred. No. 3.9e-133;
0; Mismatches 41;
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5', mRNA sequence.
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                                                                                                                                                                                                                            GAGCCCTGACTATGTGACAGAAAAGAGCATCAGCATGCTGGAGTTTAAACTGGGTGTCAT 1463
                                                                                                                                                                                                                                                                                    AAATACAGTGGAAGCAGTTTTTGATTTCATTCAGAGAAGCAGAAGGATGATTGTTGTTCT 1403
                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCGGGCTCATTTTGGAACAGATGAAACCATTTTAGATGGAAAAGAGTATGATATTTA 1223
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                                                                                                                                                      GTGCCAAAACTCCATTGCCACCAAGCTCATTGTGGTTTGAGTATCGT
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                                       mRNA sequence.
BI331848
                                                               BI331848
602982528F1 NCI_CGAP_Li9
                           BI331848.1
house mouse.
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888
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IMAGE:5135287 5',
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REFERENCE AUTHORS TITLE KEYWORDS SOURCE ORGANISM ACCESSION VERSION FEATURES COMMENT DEFINITION Snoo source Contact: KUDELL CLAND CONTACT: KUDELL CONTACT: KUDELL CONTACT: WITH CONTACT CO Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 888)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D. 888. T organism="Mus musculus"

/db\_xref="taxon:10090" /clone="IMAGE:5135287" /clone\_lib="NCI\_CGAP\_Li

\_lib="NCI\_CGAP\_Li9"

strain="FVB/N"

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                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAAAATGTAGACGGATACTTTCCTTCCAGTGTCAAACCATCGGTCACTTGGTATAAGGG
                                                                                                                                                                                BB625831 RIKEN full-length enriched, adult male diencephalon musculus cDNA clone 9330131B06 5', mRNA sequence.
                                                                                                                                                                  musculus cDNA clone
BB625831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
1 (bases 1 to 652)
Arakawa,T., Carminci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
, Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
                                                                                                  Mus musculus
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                                                                                                                                                    BB625831.1
                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                  house mouse
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/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
/Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 227 c 219 g 225 t
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Pred. No. 4.8e-1
                                                               Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                                                                    Euteleostomi;
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                                                                    Murinae;
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The Institute of Physical and Chemical Research
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaga
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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URL:http://genome.gsc.riken.go.jp/
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Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct. Func. Genomics 2 pre, L72-L86 (2001)
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                                                                                                                                 Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
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Human IL-1R ACP pr Human xrec2. Homo Human xrectein SEQ Human protein SEQ Human interleukin-Human IL-1R ACP pr Human IL-1R ACP pr Human interleukin-

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Interleukin-18 rec Human receptor pro

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Interleukin-18 rec Chicken interleuki Mouse interleukin-

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ALIGNMENTS

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Homo sapiens.		IL-1; IL-1RI; immun	IL-1R AcP; human; i		Human interleukin-1		21-MAY-2002 (first		AAU09966;		AAU09966 standard;	AAU09966	OLT 1

Human interleukin-1 Receptor accessory protein (IL-1R AcP) protein.

(first entry)

IL-1R AcP; human; interleukin-1 receptor accessory protein; NF-kappaB; IL-1; IL-1RI; immunogen; inflammatory response.

AAU09966 standard; Protein; 570

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Matches 488;
                                                                                                                                                                                                                                                                                                                                                                                                           of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-IRI and IL-IRacP as a result of protein overexpression can elicit a signaling pathway leading to NF-kappaB activation. Modulating signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity
                                                                                                                                                                                                                                    therapy, therapeutic In-leach nucleary across are availability of cellular expression or intracellular comprises a method of screening active IL-leach. This invention also comprises a method of screening an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-leach) to a binding target.
                                                                                                                                                                                                                                                                                                        of II-lRacP using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify with type and mutant II-lRacP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic II-lRacP nucleic acids are used to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein (IL-1RacP) of the invention. The interleukin receptor accessory protein (IL-1RacP) and its modulators (agonists/antagonists)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1;
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                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                      Local Similarity
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                                                                                                        MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST
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                                              AHSAGLTLIWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT
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85.3%; Pred. No. 1.4e-212;
tive 35; Mismatches 37;
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18-MAR-1998;
15-APR-1998;
10-AUG-1998;
                                                                                          Antibody fragments which specifically be receptor-like molecules are useful to tabnormal expression of the receptor or
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17-NOV-1997;
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                                                                   abnormal expression of the receptor immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1998;
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98US-078008P.
98US-078416P.
98US-081883P.
98US-095987P.
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Disclosure; Column 51-54; 102pp; English

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Best Local Similarity
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Homo sapiens
                                                                                 Human
                                                                                                                    21-MAY-2002
                                                                                                                                                                                     AAU09978 standard; Protein; 550
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                                                                                                                                                                                                                                                                                                                                                           LBFKLGVMCQNSIATK----LIVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMG
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                                                                                                                                                                                                                                                                                                                                      LELKAGL---ENMASRGNINVILVQYKAVKETK--VKELKRAKTVLTVIKMKGEKSKYPQ
                                                                                                                                                                                                                                                                                                                                                                                                           VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLSPNYVLQGTQAL
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                                                                                 IL-1R AcP protein deletion mutant delta
                               AcP; human; IL-1RI; muta
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                              interleukin-1 receptor accessory protein; NF-kappaB;
int; mutein; delta Cl; inflammatory response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.5%; Score 2586; DB 23; 85.3%; Pred. No. 1.4e-212; ative 35; Mismatches 37;
                                                                                 Ci.
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CYKIQNFNNVIPEGMNLSPLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA 240

YCSKVAFPLEVVQKDSCFNSPMKLFVHKLYIEYGIQRITCPNVDGYFPSSVKFTITWYMG 180

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1 MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDBPARIKCPLFEHFLKFNYST

MILLMCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYST

AHSAGLTLIMYMTRQDRDLEBPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120

120

60 60

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This sequence represents the human interleukin-1 receptor accessory comported (IL-1RacP) mutant delta Cl of the invention. This mutant Cl was used to define domains of the IL-1RacP protein that have the Ca ability to activate NF-kappaB expression. The interleukin receptor accessory protein (IL-1RacP) and its modulators (agonists/antagonists) Cl are useful for regulating cell function. Transient expression of either Cl IL-1RI or IL-1RAcP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 29 cells, however coexpression of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-1RI and IL-1RacP a result of protein overexpression can elicit a signaling pathway cl leading to NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IL-1RI and IL-1RacP as a result of protein overexpression can elicit a signaling pathway cl leading to NF-kappaB activation. Modulating signal transduction involving NF-kappaB in a cell may be achieved by modulating the activity of IL-1RacP using binding agents such as agonists and antagonists. Cl for IL-1RacP using binding agents such as agonists and antagonists. Cl involving NF-kappaB in a cell may be achieved by modulatify wild-type and mutant IL-1RAcP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific cligonuclectide (ASO) probes for high-throughput clinical diagnoses of therapy, therapeutic IL-1RacP nucleic acids are used to modulate callular expression or intracellular concentration or availability of active IL-1RacP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1RacP) to a binding target.

CC appearing as AAU09966 and theinformation given in table 1 of the
                                                                                      Query Match
Matches 484;
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page - ; 21pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function
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                      Local Similarity
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                                                                                      550
  Conservative
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                      70.3%; Score 2580; DB 22; 87.4%; Pred. No. 4.4e-212;
33; Mismatches
  25;
                                        Length
  Indels
  12;
Gaps
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW01911 standard;
Isolated interleukin-1 receptor accessory protein - used
prods. to treat or prevent inflammatory or immunological
of interleukin-1
                                                                                                                                                                                                                                                            Domain
                                        WPI; 1996-362691/36.
N-PSDB; AAT32026.
                                                                                                                   23-JAN-1995;
                                                                                                                                       17-JAN-1996;
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                                                                                                                                                                                                                                                                                 Protein
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GRFWKQLQVAMPVK 549
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                                                                                                                                                                                                                                                                                                                                                           leukaemia.
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21..570
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                           /label= Transmembrane_domain
                                                                                                                                                                                                                                                  'label≃
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AAU09979; 21-MAY-2002

(first

entry)

AAU09979 standard; Protein;

540 AA

IL-1R AcP; hu IL-1; IL-1RI;

mutant;

interleukin-1 receptor accessory protein; NF-kappaB;
ant; mutein; delta C2; inflammatory response.

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Human IL-1R AcP protein deletion mutant delta

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Best Local Similarity
Matches 487; Conservat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 74-75; 115pp; English.
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                                                                                                    SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVEL
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                                                                                                                                                                                                             CYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA
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WKQLQVAMPVKKSPRRSSSDEQGLSYSSL
             WKALRLALPLRSLSASSGWNESCSSQSDI
                                                 LELKAGLENMGSRGNINVILVQYKAVKETK--VKELKRAKTVLTVIKWKGEKSKYPQGRF
                                                                       LEFKLGVMCQNSIAT-KLIVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSGSKF
                                                                                                                                                                                                                                                                 VPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 AA;
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  567
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                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy, therapeutic II-IRacP nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active II-IRacP. This invention also comprises a method of screening an agent that modulates the interaction of an interleukin receptor accessory polypeptide (II-1RacP) to a binding target.

Note: The present sequence is not included in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function -
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         specification but was created from the human IL-1R AcP sequence appearing as AAU09966 and theinformation given in table 1 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents the human interleukin-1 receptor accessory protein (IL-1RacP) mutant delta C2 of the invention. This mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page - ; 21pp; English.
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CYKIQNFNNVIPEGMALSFLIALISNNGNYTCVVTYPENGRTFHLIRTLIVKVVGSPKNA
                                                                                                                                                              AHSAGLTLI WYWTTQDRDLEEP I NFRLPENR I SKEKDVLWFRPTLLADTGNYTCMLRNTT
                                                                                                                                                                                                                                             MTLLWCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYST
                                                           YCSKVAPPLEVVQKOSCENSPMKLPVHKLYIEYGIQRITCPNVDGYPPSSVKPTITWYMG
                                                                                    YCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMG
                                                                                                                                                                                                                      MTLLWCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYST
                                                                                                                                          AHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT
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Pred. No. 2.7e-210;
B; Mismatches 24;
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This sequence represents the human interleukin-1 receptor accessory protein (IL-IRacP) mutant delta C3 of the invention. This mutant was used to define domains of the IL-IRacP protein that have the ability to activate NF-kappaB expression. The interleukin receptor accessory protein (IL-IRacP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-IRI of IL-IRacP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NF-kappaB activity to a level comparable to that induced by IL-1. These data suggest that aggregation of IU-IRI and IL-IRacP as
                                                                                                                                                                                                                                       Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function
                                                                                                                                                                                                                                                                                          WPI; 2001-595441/67.
N-PSDB; AAS15608.
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IL-1;
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IL-1RI; muta
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ant; mutein; delta C; inflammatory response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 involving NF-kappaB in a cell may be achieved by modulating the activity of IL-IRacP using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant IL-IRAcP alleles in clinical and laboratory type and mutant alleles are used to generate allele-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a result of protein overexpression can elicit a signaling leading to NP-kappaB activation. Modulating signal transd
                                     Human IL-1R AcP protein deletion mutant delta N1
                                                                                                                                                AAU09973 standard; Protein;
   IL-1R AcP;
                                                                            21-MAY-2002
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                                                                                                                                                                                                                                              LELKAGL---ENMASRGNINVILVQYKAVKETK--VKELKRAKTVLTVIKWKGEK 530
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                                                                                                                                                                                                                                                                               LEFKLGVMCQNSIATK----LIVVEYRPLEHPHPGILQLKES---VSFVSWKGEK 528
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 interleukin-1 receptor accessory protein; NF-kappaB
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                                                                                                                                                                                                                                                                                                                                                                                      ct accessory protein (11-18acF) and the modulators (agonists) and operation. CC are useful for regulating ceall function, Transient expression of either CC IL-1RI or IL-1RAcP alone does not result in ligand-independent induction CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however CC coexpression of both proteins resulted in a 20-fold increase in CC attivation of NF-kappaB activity to a level comparable to that induced CC by IL-1. These data suggest that aggregation of IL-1RI and IL-1RacP as CC a result of protein overexpression can elicit a signaling pathway CC leading to NF-kappaB activation. Modulating signal transduction CC involving NF-kappaB in a cell may be achieved by modulating the activity CC of IL-1RacP using binding agents such as agonists and antagonists. CC type and mutant IL-1RAcP alleles in clinical and laboratory type and mutant IL-1RAcP alleles in clinical and laboratory colligonucleotide (AsO) probes for high-throughput clinical diagnoses CC of diseases or disorders with an inflammatory response. In C therapy, therapeutic IL-1RacP nucleic acids are used to modulate C cellular expression or intracellular concentration or availability of active IL-1RacP. This invention also comprises a method of screening for C accessory polypeptide (IL-1RacP) to a binding target. CC specification but was created from the human IL-1R AcP sequence can agpent that modulates is not included in the specific and theinformation given in table 1 of the comparisor as ANU09966 and theinformation given in table 1 of the
                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the human interleukin-1 receptor accessory protein (IL-1RacP) mutant delta N1 of the invention. This mutant
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                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                          12 FYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWY
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                                                                                                                                                                WTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRUTTYCSKVAFPLEV 131
                       VQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMGCYKIQNFNNVI 191
                                                                                  VQKDSCFNSPMKLFVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMGCYKIQNFXNVI 180
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PEGWNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDH

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RESULT 8
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           protein at tyrosine 503. The interleukin receptor accessory protein (IL-IRacP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either IL-IRI or IL-IRAcP alone does not result in ligand-independent induction of an NP-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in
                                                                               This sequence represents the human interleukin-1 receptor accessory protein (IL-1RacP) mutant delta C2 #2 of the invention. This deletimutant was used to define a phosphorylated domain of the IL-1RacP protein at tyrosine 503. The interleukin receptor accessory protein
                                                                                                                                                                              Isolated polypeptide designated interleukin receptor accessory
polypeptide is useful for regulating cell function -
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RESULT 9
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AC AAU0
XX
DT 21-1
XX
DB Huma

AAU09981

standard;

Protein;

AAU09981; 21-MAY-2002 Human IL-1R

AcP protein deletion mutant delta

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(first entry)

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                                                                                          VLTTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISM
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LEFKLGVMCQNSIATK----LIVVEYRPLE
                                                               VLLTLRGVLENERGYKLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLSPNYVLQGTQAL
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                                                                                                                                                                                                                                                                                                                                                       cc ability to activate NF-kappaB expression. The interleukin receptor cc ability to activate NF-kappaB expression. Transient expression of either care useful for regulating cell function. Transient expression of either cc are useful for regulating cell function. Transient expression of either cc II-IRI or II-IRACP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of NF-kappaB extivity to a level comparable to that induced by II-1. These data suggest that aggregation of II-IRI and II-IRACP as a result of protein overexpression can elicit a signaling pathway cc leading to NF-kappaB activation. Modulating signal transduction cr involving NF-kappaB activation. Modulating signal transduction cr involving NF-kappaB in a cell may be achieved by modulating the activity of II-IRACP using binding agents such as agonists and antagonists. Cc Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant II-IRACP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific coligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic II-IRACP nucleic acids are used to modulate cellular expression or intracellular concentration or availability of active II-IRACP. This invention also comprises a method of screening for cative II-IRACP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor specification but was created from the human II-IR AcP sequence specification.
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N-PSDB;
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                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page - ; 21pp; English. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function -
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IL-1; IL-1RI; mutant; mutein; delta C4; inflammatory response.
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                                                                                                                                                                         1 MTLLWCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEFARIKCPLFEHFLKFNYST 60
AHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRVTT
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DB; AAS15608.
                                                                           AHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT
                                                                                                                                                   HILLMCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYST 60
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92.0%;
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Pred. No. 1.8e-205;
Pred. No. 1.8e-205;
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                                           WPI; 199
N-PSDB;
Isolated interleukin-1 receptor accessory protein - used to develop prods, to treat or prevent inflammatory or immunological activities of interleukin-1
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                                                                                                                         23-JAN-1995;
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                                            1996-362691/36.
DB; AAT32028.
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Matches 429
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                                                                                  Mouse interleukin-1 Receptor accessory protein (IL-1R AcP) protein
              Mus sp.
                                        II-1R AcP; mouse; interleukin-1 receptor accessory protein; NF-kappaB;
IL-1; IL-1RI; inflammatory response.
                                                                                                                    21-MAY-2002
                                                                                                                                                                              AAU09967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC protein (II-IR AcP), the cDNA sequence for this protein was used to generate a hybridisation probe that was used to isolate the human CC II-IR AcP cDNA sequence of the invention. The interleukin-1 receptor CC accessory protein (II-IR AcP) and its modulators (agonists/antagonists) are useful for regulating cell function. Transient expression of either CI II-IR or II-IR AcP alone does not result in ligand-independent induction of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in CC activation of NF-kappaB activity to a level comparable to that induced by II-1. These data suggest that aggregation of II-IRI and II-I RACP as a result of protein overexpression can elicit a signaling pathway CC leading to NF-kappaB activation. Modulating signal transduction CC involving NF-kappaB in a cell may be achieved by modulating the activity of II-IRACP using binding agents such as agonists and antagonists. CC Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant II-IR AcP alleles in clinical and laboratory CC samples. Mutant alleles are used to generate allele-specific CC digonucleotide (ASO) probes for high-throughput clinical diagnoses CC of diseases or disorders with an inflammatory response. In CC cellular expression or intracellular concentration or availability of CC active II-IR ACP. This invention also comprises a method of screening for an agent that modulates the interaction of an interleukin receptor CC accessory polypeptide (II-IRACP) to a binding target.
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N-PSDB;
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                                                                                           CYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA 240
                                                                                                                                                                   YCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMG 180
                                                                                                                                                                                                                                                   AHSAGLTLIWYWTRQDRDLEBPINFRLPENRISKEKDVLWFRPTILLNDTGNYTCMLRNTT 120
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                                                                                                                                                                                                                             AHSSGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
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DB; AAS15609.
LPPQIYSPNDRVVYEKEPGEELVIPCKVYFSFIMDSHNEVWWTIDGKKPDDVTVDITINE
                                                                         CTEIVDFHNVLPEGMNLSFFIPLVSNNGNYTCVVTYPENGRLFHLTRTVTVKVVGSPKDA
                                                                                                                                                   YCSKVAFPLEVVQKDSCFNSAMRPPVHKMYIEHGIHKITCPNVDGYFPSSVKPSVTWYKG 180
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18-MAR-1998;
15-APR-1998;
The present invention relates to compositions and methods for affect: mammalian physiology such as morphogenesis of immune system function. The invention particularly relates to nucleic acids, proteins and antibodies which regulate development and/or the immune system. The invention also relates to antibody fragments which specifically bind to antigenic fragments of a primate interleukin (IL)-1 receptor like
                                                                                        Antibody fragments which specifically bind to primate interleukin receptor-like molecules are useful to treat conditions associated abnormal expression of the receptor or its ligand, particularly immunological disorders
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                                                                      Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                  protein; therapy; immunological disorder.
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IL-1; IL-1R
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                                                                                                                                                                                                                                                        IL-1R
                                                                                                                                                                                    IL-1RI;
                                                                                                                                                                                    human; interleukin-1 receptor accessory protein; NF-kappaB; RI; mutant; mutein; delta N2; inflammatory response.
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Pred. No. 2e-190;
6; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accessory protein (II-IRacP) and its modulators (agonists) are useful for regulating cell function. Transient expression of either II-IRI or II-IRAcP alone does not result in ligand-independent induction of an NW-kappaB-dependent luciferase reporter gene in 293 cells, however coexpression of both proteins resulted in a 20-fold increase in activation of NW-kappaB activity to a level comparable to that induced by II-1. These data suggest that aggregation of II-IRI and II-IRacP as a result of protein overexpression can elicit a signaling pathway leading to NW-kappaB activation. Modulating signal transduction involving NW-kappaB in a cell may be achieved by modulating the activity of II-IRacP using binding agents such as agonists and antagonists. Hybridisation probes to the cDNA sequence can be used to identify wild-type and mutant II-IRACP alleles in clinical and laboratory samples. Mutant alleles are used to generate allele-specific oligonucleotide (ASO) probes for high-throughput clinical diagnoses of diseases or disorders with an inflammatory response. In therapy, therapeutic II-IRACP nucleic acids are used to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cellular expression or intracellular concentration or availability of active IL-1RacP. This invention also comprises a method of screening an agent that modulates the interaction of an interleukin receptor accessory polypeptide (IL-1RacP) to a binding target. Note: The present sequence is not included in the specification but was created from the human IL-1R AcP sequence appearing as AAU09966 and theinformation given in table 1 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the human interleukin-1 receptor accessory protein (IL-1RacP) mutant delta N2 of the invention. This mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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N-PSDB; AAS15608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               was used to define domains of the IL-1RacP
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GPGATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEEEVL
                                                                                                                                                               PVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKFDDITIDVTINESI
                                                                                                                                                                                                                                              KIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVP
                                                                                                                                                                                                                                                                                                                          SKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMGCY
                                                                                                                                                                                                                                                                                                                                                                             SAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDYLWFRPTLLNDTGNYTCMLRNTTYC
                                                                                   SHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELAC
                                                                                                                                                                                                                      KIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVP
                                                                                                                                                                                                                                                                                                   SKVAPPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMGCY
                                                             SHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELAC
                                                                                                                                            PVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINESI
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Pred. No. 3e-183;
35; Mismatches 3
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CC (II-IRACP) and its modulators (agonists/antagonists) are useful
CC (II-IRACP) and its modulators (agonists/antagonists) are useful
CC or II-IRACP alone does not result in ligand-independent induction
CC of an NF-kappaB-dependent luciferase reporter gene in 293 cells, however
CC coexpression of both proteins resulted in a 20-fold increase in
CC activation of NF-kappaB activity to a level comparable to that induced
CC by II-1. These data suggest that aggregation of II-IRI and II-IRacP as
CC a result of protein overexpression can elicit a signaling pathway
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC involving NF-kappaB in a cell may be achieved by modulating the activity
CC if II-IRacP using binding agents such as agonists and antagonists.
CC type and mutant II-IRACP alleles in clinical and laboratory
CC samples. Mutant alleles are used to generate allele-specific
CC oligonucleotide (ASO) probes for high-throughput clinical diagnoses
CC of diseases or disorders with an inflammatory response. In
CC cellular expression or intracellular concentration or availability of
CC active II-IRacP. This invention also comprises a method of screening for
                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human interleukin-1 receptor accessory protein (IL-1RacP) mutant delta N1 #2 of the invention. This deletic mutant was used to define a phosphorylated domain of the IL-1RacP protein at tyrosine 503. The interleukin receptor accessory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated polypeptide designated interleukin receptor accessory polypeptide is useful for regulating cell function
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page - ; 21pp; English
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                                                                                                                                                                                                                                                                                   AAW01912 standard; Protein; 359
                                                                                                               cancer; leukaemia.
                 Domain
                                                                                   Synthetic.
                                                                                                                           Interleukin-1 receptor accessory protein; IL-1 antagonist; inflammation; therapy; antiinflammatory; antibody; rheumatoid arthritis; inflammatory bowel disease; septic stransplant rejection; psoriasis; asthma; type 1 diabetes;
                                            Peptide
                                                                                                                         rheumatoid arthritis;
transplant rejection;
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es 419; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVVILIVVYHVYMLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEEFVLLTLRGVL 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVVQKDSCFNSPMKLPVHKLYIEYGIQRITCDNVDGYFPSSVKPTITWYMGCYKIQNFNN 189
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 /label= Sig_peptide
21..359
/label= Extracellul
                                                      Location/Qualifiers
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83.3%; Pred. No. 1.3e-180;
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Extracellular_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated interleukin-1 receptor accessory protein - used prods. to treat or prevent inflammatory or immunological of interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   disease, septic shock, transplant rejection, psoriasis, asthma, type 1 diabetes or acute and chronic myelogenous leukaemia, and can also be used to screen potential IL-1 antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A soluble form (AAW01912) of human interleukin-1 receptor accessory protein (IL-1R ACP) (AAW01911) lacks the transmembrane
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VPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300
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Search completed: April 23, 2003, 08:51:43
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Listing first 45 summaries
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgm2_6/ptodata/1/iaa/5B_COMB.pep:*
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Sequence 2, Appli	Sequence 2, Appli	Sequence 31, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 22, Appl	Sequence 2, Appli	Sequence 14, Appl	Sequence 16, Appl	Sequence 23, Appl	Sequence 4, Appli	Sequence 8, Appli	Sequence 10, Appl	Sequence 39, Appl	Sequence 24, Appl

## ALIGNMENTS

US-08-991-944-2

Application US/08991944

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Patent No. 6280959
                                                                                                                          Matches 488;
                                                                                                                                                           Query Match
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: 4
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Interleu
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                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                       Match 70.5%;
Local Similarity 85.3%;
                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/991,944
AHSAGLTLIWYWTRQDRDLEBPINFRLPENRISKEKDYLWFRPTLLINDTGNYTCMLRNTT 120
                                                   MTLLWCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYST
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                                                                                                                        35; Mismatches
                                                                                                                                     Score 2586; DB 4;
Pred. No. 2.8e-244;
                                                                                                                                                                                                                                                                                                                                                                         T97-014
                                                                                                                                                           Length 570;
                                                                                                                          Indels 12;
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US-09-173-151A-36
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APPLICANT: Timans
APPLICANT: Debets
                                                                                                                    FILING DALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/065,776
                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/173,151A FILING DATE: 14-CCT-1998
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
NUMBER OF SEQUENCES: 36
     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-APR-
                                                                                         APPLICATION NUMBER: US 6
FILING DATE: 17-NOV-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
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                                                         APPLICATION NUMBER: US 6
FILING DATE: 12-MAR-1998
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Debets, Johannes Eduard Maria
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     MBER: US 60/081,883
15-APR-1998
                                                                              US 60/078,008
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RESULT 3
US-08-991-944-4
; Sequence 4, Application US/08991944
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Best Local Similarity 85.3%;
Matches 488; Conservative 35
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-AUG-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
PILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/
PILING DATE: 15-OCT-1997
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REGIESTATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
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                                                                                             GRFWKQLQVAMPVKKSPRRSSSDEQGLSYSSL
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, Edwin P.
, 34,090
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Pred. No. 2.8e-244;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 570 amino acids
TYPE: amino acid
TYPE: amino acid
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MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cao, Zhaodan
TITLE OF INVENTION: Interleukin-1 Receptor Accessory Proteins,
TITLE OF INVENTION: Nucleic Acids and Methods
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: T97-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                              301
                                         421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTLLMCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYST 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                          LPPQIYSPNDRVVYEKEPGEELVIPCKVYFSFINDSHNEVWWTIDGKKPDDVTVDITINE 300
                                                                                                                                                                                                                                                                                                                                            CYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA 240
                                                                                                                                                                                                                                                                                                                                                                                                                         YCŚKVAFPLEVVQKDSCFNSPMKLPVHKLYĮEYGIQRITCPNVDGYFPSSVKPTITWYMG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGLLWYLMSLSFYGILQSHASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKYNYST 60
                                                                                                                                                          SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVEL 360
VILTLRGVLENBFGYKLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLSPNYVLQGTQAL 480
                         VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISM 480
                                                                                                ACGFGATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEEF 420
                                                                                                                                                                                                                                                                                                                         CTEIVDFHNVLPEGMNLSFFIPLVSNNGNYTCVVTYPENGRLFHLTRTVTVKVVGSPKDA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHSSGLTLIWYWTRODRDLEEPINFRLPENRISKEKDVLWPRPTLLNDTGNYTCMLRNTT 120
                                                                             ACGFGATVFLVVVLIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNVEEEEF
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T: 75 DENISE DRIVE
HILLSBOROUGH
CALIFORNIA
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Patent No. 632647
                                                                                      TELEFAX: (650) 496-1200
INFORMATION FOR SEQ ID NO: -21:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                        REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 APPLICATION NUMBER: US 60
FILING DATE: 15-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
PRIOR APPLICATION NUMBER: US 60/078,008
APPLICATION NUMBER: US 60/078,008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,151A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
COERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-APR-PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                      TOPOLOGY:
                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 14-OCT
                                  STRANDEDNESS:
                                                                                                                                                          TELEPHONE:
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                                                                              ENGTH:
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Debets, Johannes Eduard Maria
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                                                                                                                                                            (650)852-9196
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15-APR-1998
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peptide
                                    not relevant
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US-09-173-151A-4
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods
                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
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                                                                                                                                                                                                                                   STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
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APPLICATION NUMBER: US/09/173,151A FILING DATE: 14-OCT-1998 CLASSIFICATION: 435
                                                                                                                                                                                               ZIP: 94304-1104
                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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Debets, Johannes Eduard Maria
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                                                                                                                                                                                                                                                                                                     DNAX Research Institute
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                                                                                   Version
                                                                                     #1.30
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NAME: Ching, Edwin F.

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX07
TELECOMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
THE COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 686 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 18-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 DVVWYKECKPKMWRSIIIQKGNALLIQEVQEEDGGNYTCELKY--EGKL--VRRTTELKV
                    453 AVFDFIQRSRRMIVVLSPDYVTEKSISMLEFKLGVMCQNSIAT---KLIVVEXRPLEHPH
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459 DLTRYVEQSRRLIIVLTPDYILRRGWSI--FELESRLHNMLVSGEIKVILIECTELK---
                                                                                                                                  402 GKEYDIYVSYAR------NAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVB
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                                                                                                                                                                                                                 342 AKAAKVKQKVPAPRYTVELACGFGATVLLVVILLIVVYHVYWLEMVLFYRAHFGTDETILD
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                                                                                                          399
                                                                                                                                                                                                                                                                                                                                                                    232 TALLIDKPPKPLFPMENOPSVIDVQLGKPLNIPCKAFFGFSGESGPMIYW-MKGEK----
                                                                                                                                                                                                                                                                                                                                                                                                          234 VGSPKNAVP-PVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDI 292
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                                                                                                                                                                                                                                                                                 ----FIEELAGHIR-EGEIRLLKEHLGEKEVELALIFDSVVEADL-ANYTCHVENRNGR-
                                                                                                                                                                                                                                                                                                                       TIDVTINESISHSRTEDETR------TQILSIKKVTSEDLKRSYVCHARSAKGEV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYCMKVSMSLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCPDMDDFKKSDQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAQSTGLRLMWY -- KNKGDLEEPIIF--SEVRMSKEEDSIWFHSAEAQDSGFYTCVLRNS
                                                                                                          NKEYDAYLSYTKVDQDTLDCDNPEEEQFALEVLPDVLEKHYGYKLFIPBRDLIPSGTYMB
                                                                                                                                                                                           - KHAS VLLRKKDLIYKIELAGGLGAIFLLLVLLVVIYKCYNIELMLFYRQHFGADETNDD
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Patent No.
                                                                          NFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/065,776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                           SEQUENCE CHARACTERISTICS
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                                                                                                                   TELECOMMUNICATION INFORMATION
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COLECULE TYPE:
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                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 6
FILING DATE: 17-NOV-1997
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                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                       650) 852-9196
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
            ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                 COUNTRY:
                                                                                                                                                   CITY: Palo Alto
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITIDVTINESISHSRTEDETR------TQILSIKKVTSEDLKRSYVCHARSAKGE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVGSPKNAVP-PVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STYCMKVSMSLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCPDMDDFKKSDQE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTYCSKVAFPLEVVQKDS--CFNSPMKLPVHKLYIEYG----IQRITCPNVDGYFPSSVK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STAQSTGLRLMWY--KNKGDLEEPIIF--SEVRMSKEEDSIWFHSAEAQDSGFYTCVLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STAHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLTRYVEQSRRLIIVLTPDYILRRGWSI--FELESRLHNMLVSGEIKVILIECTELK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VEAVEDEIORSRRMIVVLSPDYVTEKSISMLEFKLGVMCQNSIAT---KLIVVEYRPLEH 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGKEYDIYVSYAR------NAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --KHASVLLRKKDLIYKIELAGGLGAIFLLLVLLVVIYKCYNIELMLFYRQHFGADETND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTALLTDKPPKPLFPMENQPSVIDVQLGKPLNIPCKAFFGFSGESGPMIYW-MKGEK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDVVWYKECKPKMWRSIIIQKGNALLIQEVQBEDGGNYTCELKY--EGKL--VRRTTELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVK 232
                                                                                                                                                                                                                                                                                                                                                                                                                                     5, Application US/09173151A
6326472
APPLICATION DATA:
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                                                                                                                                                                                             901 California Avenue
                                                                                                                                                                                                                                                                                         Bazan, J. Fernando
Kastelein, Robert A.
                                                                                                                                                                                                                                                                                                                                                                         Timans,
Debets,
                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                  Sana, Theodore R.
                                                                                                                                                                                                                                                                                                                                                         Antonius
                                                                                                                                                                                                               DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                       Jacqueline C.
Johannes Eduard
                                                                                                                                                                                                                                                                         Human Receptor Proteins; Related Reagents and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.8%; Score 800; DB 4; 35.1%; Pred. No. 2.1e-69;
                Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96; Mismatches 208;
                  Version #1.30
                                                                                                                                                                                                                                                                                                                                                                           Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650)496-1200 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/078,416
FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                              402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 MK-----YFEKAELSKSKBISCRDIEDFLLPTREPEILWYKECRTKTWRPSIVFKRDTL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 MKLPVHKLYIEYG----IQRITCPNVDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNL 197
                                                                                                                                                                                                                                                                                                                229 TQLGDSANLTCRAFFGYSGDVSPLIYWMKGEKFIEDLDENRVWESDIRI---LKEHLGEQ 285
                                                                                                                                                                                                                                                                                                                                                        256 KEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDI-----TIDVTINESISHSRTED 309
                                                                                                                                                                                                                                                                                                                                                                                                    174 LIREVREDDIGNYTCELKY--GGFVVRRTTELTVT---APLIDKPPKILLYPMESKLTIQE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 SFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDH--VVYE 255
481 LEFKLGVMCQNSIAT---KLIVVEYRPLEHPHPGILQLKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AF--DGSRMSKEEDSIWFRPTLLQDSGLYACVIRNSTYCMKVSISLTVGENDTGLCYNSK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 NFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDS--CFNSP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 CDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEEFI 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ching, Edwin E REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                      VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISM 480
                                                                                                                                                                          LVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYAR------NAEEEEF 420
                                                                                                                                                                                                                         EVSISLI-VDSVEEGDL-GNYSCYVENGNGR--RHASVLLHKRELMYTVELAGGLGAILL 341
                                                                                                                                                                                                                                                                   ETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELACGFGATVL 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTDWSID-IKKYQVLVGEPVRIKCALFYGYIRTNYSLAQSAGLSLMWYKSSGPGDFEEPI 61
                                                                                                                                LLVCLVTIYKCYKIEIMLFYRNHFGAEELDGDNKDYDAYLSYTKVDPDQWNQETGEEERF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   668 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.8%; Score 762.5; DB 4; ilarity 29.7%; Pred. No. 1.3e-65; Conservative 119; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (650) 852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JMBER: US 60/062,066
15-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 91; Gaps
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---SVSFVSWKGEK 528
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121 YCSKVAFPLEVVQ--KDSCFN----SPMKLPVHKLYIBYGIQRITCPNVDGYFPSSVKPT 174

Q----KWKLNVIRRNKHSCFTERQVTSKIVEVKKFF---

ITWYMGCYKIQNFNNVIPB-GMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKV

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                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-604-333-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Apr. No. 5776731
                                                                                                                            Matches 174;
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Microsoft Wo
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 5.
STREET: 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     576 HPDLRSTFHNTYHSOMROKHYYRSYEYDV--PPTGTLPLTSIGNOHTYCNIPMTLINGOR 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 CNKLNSKFWKRLQYEMPFKRIEPITHEQALDVSEQGPFGELQTVSAISMAAATSTALATA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 PQTKSSREQNPDEAHTNSAILPLLPRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529 SKHSGSKFWKALRLALPLR-----
 47
                             62
                                                                                                                                                                                                                        TOPOLOGY:
                                                             10 LWVLISV-----STAESC-----TSRPHITVVEGEPFYLKHC-----SCSLA
                                                                                                                                                                                                                                                                                                                                                                                    NAME: Anderson, Kath
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 21-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                             4 LWCVVSLYFYGILQSDASERCDDWGLDTMR-QIQVFEDEPARIK-CPLFEHFLKFNYSTA 61
HEIETTTKSWYKSSGSQEHVE-LNPR-SSSRIALHDCVLEFWPVELNDTGSYFFQMKNYT
                             HSAGLTL-IWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVQRR-----RSRLKEPPELQSSERAAGSPPAPGXMSKHRGKSSATCRCCVTYCEGEN 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98101
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                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 University Street
                                                                                                                                                                                                                                                                                                                     (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                            Conservative
                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Floppy disk
Apple Macintosh
YSTEM: Apple 7.1
Microsoft Word, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kathryn A.
                                                                                                                                                                                                                                                                                                                                      (206) 587-0430
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ORMATIO...
32,172
32,172
2619
                                                                                                                                          14.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/604,333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson,
                                                                                                                                                                                                                                                                                       2
                                                                                                                            93;
                                                                                                                                          Score 528; DB 1;
Pred. No. 8.2e-43;
                                                                                                                            Mismatches
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                                                                                                                                                       Length 541;
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                                             ; MOLECULE TYPE:
US-09-110-618-2
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08
APPLICATION NUMBER: US/08
APPLICATION NUMBER: US/08
                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft WC
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Parnet, TITLE OF INVENTION:
                                                                                                                                                                                                          NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REPERENCE/DOCKET NUMBER: 2619
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346
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                                                                                    TOPOLOGY:
                                                                                                                                                                                        TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Apple Macintosh
                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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51 University
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                                                                                                                                                                                            (206) 233-0644
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14.4%;
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Street
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Score 528;
Pred. No.
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 8.2e-43;
                Length 541;
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US-09-173-151A-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Timans
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                          ZIP: 94304-1104
COMPUTER READABLE FORM:
PRIOR APPLICATION DATA:
                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Human Receptor Proteins; Related NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                              APPLICATION NUMBER: US/0 FILING DATE: 14-OCT-1998
                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47
                 CLASSIFICATION:
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 HSAGLTL-IWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LWCVVSLYFYGILQSDASERCDDWGLDTMR-QIQVFEDEPARIK-CPLFEHFLKFNYSTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TILDGKEYDIYYSYAR-----NABEBEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVE 452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEDRSNIVPVLLGPKLNHVAVEL--GKNVRLNC----SALLNEEDVIYMMFGEENGSDPN 260
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                                                                                                                                                                                                                                      T: 901 California
Palo Alto
                                                                                                                                                                                                                   California
                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                 Sana, Theodore R. Bazan, J. Fernando
                                                                                                                                                                                                                                                                                                                                                                                                                     Timans, Jacqueline C.
Debets, Johannes Eduard Maria
                                                                                                                                                                                                                                                                                                                                                Kastelein, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                     Antonius
                                                                                                                                                                                                                                                                        DNAX Research Institute
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                                                     US/09/173,151A
                                                                                                                                                                                                                                                         Avenue
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APPLICATION NUMBER:

US 60/065,776

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MOLECULE TYPE:
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APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
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                                                                                                398 TILDGKEYDIYVSYAR-----NAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVE 452
                                                                                                                                                    312 ILVRKADMADIPGHVFT----RGMIIAVLILVAVVCLVTVCVIYRVDLVLFYRHLTRRDE
                                                                                                                                                                                        346 KVKQK-----VPAPRYTVELACGFGATVLL---VVILIVVYHVYWLEMVLFYRAHFGTDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YCSKVAFPLEVVQ--KDSCFN----SPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPT 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 HSAGLTL-IWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q----KWKLNVIRRNKHSCFTERQVTSKIVEVKKFF-----QITCEN--SYYQTLVNST
EIHSLIEKSRRLIIVLSKSYMSNEVRYELESGLHEALVERKI--KIILIEFTPVTDFTFL
                                      AVFDFIQRSRRMIVVLSPDYVTEKSISMLEFKL-GVMCQNSIATKLIVVEYRPLEHPH--
                                                                                                                                                                                                                                                                  IDVTINESISHSRTEDETRT-----QILSIKKVTSEDLKRSYVCHARSAKGEVAKAA 345
                                                                                                                                                                                                                                                                                                        VEDRSNIVPVLLGPKLNHVAVEL--GKNVRLNC----SALLNEEDVIYMMFGEENGSDPN 260
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                                                                                                                                                                                                                                                                                                                                          VGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDIT
                                                                        TLTDGKTYDAFVSYLKECRPENGEEHTFAVEILPRVLEKHFGYKLCIFERDVVPGGAVVD
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(650) TN NO: 28:
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Pred. No. 8.2e-43;
3; Mismatches 215;
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US-09-578-178-2
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
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NAME: Anderson, Kathryn
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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                             VGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDIT 293
                                                                                                 ITWYMGCYKIQNFNNVIPE-GMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKV 233
                                                                                                                                        Q----KWKLNVIRRNKHSCFTERQVTSKIVEVKKFF-----QITCEN--SYYQTLVNST
                                                                                                                                                                       YCSKVAFPLEVVO--KDSCFN----SPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPT 174
                                                                                                                                                                                                            HEIETTTKSWYKSSGSQEHVE-LNPR-SSSRIALHDCVLEFWPVELNDTGSYFFQMKNYT 104
                                                                  -SLYKNCKKLLLENNKNPTIKKNAEF-----EDQGYYSCVHFLHHNGKLFNITKTFNITI
VEDRSNIVPVLLGPKLNHVAVEL--GKNVRLNC---
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51 University Street
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Receptor Designated:
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                                                                                                                                                                                                                                                                                                                                                   14.4%; Score 528; DB 4; 30.0%; Pred. No. 8.2e-43; tive 93; Mismatches 215;
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   SALLNEEDVIYWMFGEENGSDPN 260
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                                                                 ; MOLECULE TYPE: US-08-996-338-20
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                Query Match
Best Local Similarity
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   Matches 167;
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                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: JP 2
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP 74,697/1997 FILING DATE: 12-MAR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DEC-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: JP 2
FILING DATE: 28-JUL-1997
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
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                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 2
                                                                                                       TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
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KURIMOTO, Musashi
VENTION: POLYPEPTIDES
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                14.2%; Score 520; DB 3; 30.5%; Pred. No. 4.7e-42;
                                                                                                                                                                                                                                                                                                                                 JP 291,837/1997
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 89; Mismatches
                                                                                                                                                                                                                                              TORIGOE=3
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 209; Indels
                                Length 521;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 6326472
GENERAL INFORMATION:
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                             CLASSIFICATION:
                                                                               FILING DATE:
                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1104
                                                                                                                                                                                                                                                                                                 CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEALVERKI -- KIILIEFTFVTDFTFLFQSLKLLKSHRVLKWKADKSLSYNSRFWKNLLY 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQ--KDSCFN----SPMKLPV 146
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                                                                                                                                                                                                                                                                           California
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                                                                                                                                                                                                                                                                                                                    901 California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antonius
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Debets, Johannes Eduard
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                                                                                               US/09/173,151A
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PRIOR APPLICATION DATA:
US 60/078,008

PRIOR APPLICATION DATA:

FILING DATE:

12-MAR-1998

APPLICATION NUMBER:

US 60/081,883

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507 YVKQKYGAIRWTGDFSERSHSASTRFWKKVRYHMPSRKHGSSSGFHLS

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; MOLECULE TYPE: peptide US-09-173-151A-32
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650)496-120
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
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514 QLKESVSFVSWKG---EKSKHSGSKFWKALRLALPLRSLSASSGWNES : | : | : | : : | : | : | : | : |
                                                                                                                                                                                                                                                                                           33 PVQNIRGYLIGGGISLIFLLELILIVYKIFKIDIVLWYRSSCHPLLGKKVSDGKIYDAYV
                                                                                                                                                                                                                                                                                                                                                  352
                                                                                                                                                                                                                                                                                                                                                                                                       278
                                                                                                                                                                                    393 LYPKNRESCLYSSDIFALKILPEVLERQCGYNLFIFGRNDLAGEAVIDVTDEKIHQSRRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 MRPEFIY-PNNNTI-EVELGSHVVMECNVSSGVYGLL-----PYWQVNDEDVD--SFDS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 AVPPVIHSPNDHVVYEKEPGEELLIPCTV---YFSFLMDSRNEVWWTIDGKKPDDITIDV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 K--IQNFNNVIPEGMN-LSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKN 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 IINLKVFKNDNGLCFNGEMK--YDQIVKSANAGKIICPDLENFKDEDNINPEIHWYKECK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 AFPLEVVQKDS--CFNSPMKLPVHKLYIEYGIQRITCPNVDGY-FPSSVKPTITWYMGCY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55 YNLTWY--RNGSNM--PITTE-RRARIHORKGLLWFIPAALEDSGLYECEVRSLNRSKOK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 LTLIWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 CVICNYP--
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STRANDEDNESS: no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 CVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAG
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                                                                                                                                                                                                                                 SYARNAE-----EEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRM 464
                                                                                                                                  IVVLSP-----DYVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLE---HPHPGIL 513
                                                                                                                                                                                                                                                                                                                                             PAPRYTVELACGFGATVLLVVILIVVYHVYWLEMVLFYRA--HFGTDETILDGKEYDIYV 409
                                                                                                                                                                                                                                                                                                                                                                                                    TYREQFYEEGMPHGIAVSGTK---FNISEVKLKDYAYKFFCHFIYDSQEFTSYIKLEH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-----INESISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKV 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGFLEDKRLVLAEGENAILILNVTIQDKGNYTCRMVYTYMGKQYNVSRTMNLEVKESPLK 227
                                                                                IIILVPEPSCYGILEDASEKHLAV----YNALIODGI--KIILIELEKIEDYANMPESIK 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         555 amino acids
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18-MAR-1998
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Pred. No. 1.2e-39;
Pred. No. 1.2e-39; Indels
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US-07-821-716-4
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Patent No. 5319071
                                                                                                                                                                                                                     Matches 153;
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Dower,
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 576 amino acid
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 125627
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CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 2:
FILING DATE: 13-OCT-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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127
                                 140 SPMKLPVHKLYIEYGIQRITCPNVDGYF--PSSVKPTITWYMGCYKIQNFNNVIPEGMNL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Wight, Christopher L. REGISTRATION NUMBER: 31,680
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Washington
                                                                                                      82 PINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDS--CFN 139
                                                                                                                                           21 EIDVCTEYPNQIVLELSVNEIDIRKCPLTPNKWH------GDTIIWY----KNDSKT 67
                                                                                                                                                                                34 QIQVFEDEPARI-------KCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
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TQATFP-QRLHİA-GDGSLVCPYV-SYFKDENNELPEVQWYKNC-KPLLLDNVSFFGVKD 182
                                                                     PISAD-RDSRIHQQNEHLWFVPAKVEDSGYYYCIVRNSTYCLKTKVTVTVLENDPGLCYS 126
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Sims, John
Grandl, David L.
Soluble
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                                                                                                                                                                                                                   13.2%; Score 484.5; DB 1; 25.8%; Pred. No. 1.7e-38; tive 120; Mismatches 225;
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                                                                                                  INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                   CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Gould, Jr., Lewis F.
REGISTRATION NUMBER: 25,057
REFERENCE/DOCKET NUMBER: 1990
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 575-6000
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                          SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/381,603
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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  MOLECULE TYPE:
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                                                      LENGTH:
                    TOPOLOGY:
                                                                                                                                       TELEPAX:
                                                                                                                                                                                                                                                                                              FILING DATE:
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1700 Market Street Suite 3232
                                                                                                                                     (215) 575-6015
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Query Match

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                                                                                                                                                                                                   BFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPD-----
                                                                                                                                                                                                                                                                                                                           KRKYTLITTLNISEVKSQFYRYPFICVVKNT--NIFESAHVQLIYPVPDFKNYLIGGFII 347
                                                                                                                                                                                                                                                                                                                                                                                                                                          KEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINES-----ISHSRT 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFLIALIS--NNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYB 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOATFP-ORLHIA-GDGSLVCPYV-SYFKDENNELPEVOWYKNC-KPLLLDNVSFFGVKD 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIDVCTEYPNQIVLFLSVNEIDIRKCPLTPNKMH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QIQVFEDEPARI------KCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEB 81
FQERPQSAKTRFWKNLRYQMPAQRRS----PLSKHRLLTLDPVRDTKEKL
                                       -- EKSKHSGSKFWKALRLALPLRSLSASSGWNESCSSQSDISLDHVQRRRSRL
                                                                             GOSSEEQIAI ----YNALIQEGI --KIVLLELEKIQDYEKMPDSIQFIKQKHGVICWSGD
                                                                                                                     -YVTEKSISMLBFKLGVMCQNSIATKLIVVEYRPLE--HPHPGILQ-LKBSVSFVSWKG- 526
                                                                                                                                                             TFVFKLLPEVLEGQFGYKLFIYGRDDYVGEDTIEVTNENVKKSRRLIIILVRDMGGFSWL
                                                                                                                                                                                                                                                                                 TVLLVVILIVVYHVYWLEMVLFYRAHFG--TDETILDGKEYDIYVSYARNAEE-----E
                                                                                                                                                                                                                                                                                                                                                                 EDE-TRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELACGFGA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPMKLPVHKLYIEYGIQRITCPNVDGYF--PSSVKPTITWYMGCYKIQNFNNVIPEGMNL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PISAD-RDSRIHQQNEHLWFVPAKVEDSGYYYCIVRNSTYCLKTKVTVTVLENDPGLCYS 126
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/ative 120;
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                                          577
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Search completed: April 23, 2003, 08:55:30 Job time : 34 secs

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Result
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length: 2000000000
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3669
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                                                      70.3
63.4
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Listing first 45 summaries
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-6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
-6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
-6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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-6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
-6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
-6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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US-09-935-868-28

US-09-935-868-28

US-10-011-548-3

US-10-011-548-35

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US-10-011-548-36
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2 US-10-157-447-2
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Sequence 21, Appli
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252		252			314				424.5									457						471.5		
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398	398	398	217	410	410	70	481	486	569	569	569	467	562	562	610	614	614	561	561	556	580	599	599	599	599	
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Sequence 2, Appli	26	Sequence 2, Appli	Sequence 11, Appl	Sequence 13, Appl	Sequence 27, Appl	Sequence 48704, A	Sequence 655, App	Sequence 20, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 31, Appl	Sequence 8, Appli	Sequence 13, Appl			Sequence 16, Appl	Sequence 2, Appli	Sequence 15, Appl	Seguence 23, Appl	•	Sequence 8, Appli	Sequence 2, Appli	10	Sequence 7, Appli	Sequence 2, Appli	

## ALIGNMENTS

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Sequence 36, Application US/100 Publication No. US20030055218A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PECENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/011,548 FILING DATE: 22-Oct-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 901 California Avenue
CITY: Palo Alto
                  APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998
                                                             APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
                                                                                                                                                       FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                         APPLICATION NUMBER: 09/173,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94304-1104
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                                                                                                           RESULT 2
                                          Sequence 4, Application US/10215211
Publication No. US20030049255A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fatches 488;
 APPLICANT: Sims, John E. APPLICANT: Smith, Dirk TITLE OF INVENTION: INTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 36: SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEPAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST
                                                                                                                                                         GRFWKQLQVAMPVKKSPRRSSSDEQGLSYSSL
                                                                                                                                                                                       SKFWKALRLALPLRSLSASSGWNESCSSQSDI
                                                                                                                                                                                                                   LEFKLGVMCQNSIATK----LIVVEYRPLEHPHPGILQLKES---VSFVSWKGEKSKHSG 533
                                                                                                                                                                                                                                                                                   VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLSPNYVLQGTQAL
                                                                                                                                                                                                                                                                                                                 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 6 FILING DATE: 15-OCT-1997
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Dirk E.
: INTERLEUKIN-1
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85.3%;
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; Pred. No. 4.2e-200;
35; Mismatches 37;
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RECEPTORS
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TREATMENT OF
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US-10-011-548-21
; Sequence 21, Application US/10011548
; Publication No. US20030055218A1
; GENERAL INFORMATION:
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US-10-215-211-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/310,789
PRIOR FILING DATE: 2001-08-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loc
Matches
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     APPLICANT:
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Timans, Jacqueline C.
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NUMBER OF SEQUI

SEQUENCES: 36 DENCE ADDRESS: ç

INVENTION: Human Receptor

Proteins;

Related Reagents

Methods

Antonius Sana, Theodore R. Bazan, J. Fernando Kastelein, Robert A. Debets, Johannes Eduard

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Best Local Similarity
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                    301
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NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVEL
                                                  CYKIQNENNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSEKNA 240
                                                                                                                                                                                                      YCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMG
                                                                                                                                                                                                                                                       AHSSGLTLIWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
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                                                                                                                                                                                                                                                                                                                       MGLLWYLMSLSFYGILQSHASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHPLKYNYST 60
                                                                                                                                                                                                                                                                                                                                         MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST 60
                                                                                                                      CTEIVDFHNVLPEGMNLSFFIPLVSNNGNYTCVVTYPENGRLFHLTRTVTVKVVGSPKDA
                                                                                                                                                                                      YCSKVAFPLEVVQKDSCFNSAMRFPVHKMYIEHGIHKITCPNVDGYFPSSVKPSVTWYKG
                                                                                                                                                                                                                                                                                                                                                                                          429;
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FILING DATE: CUNKNOWN
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 570 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030055218A1 Relevant
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/078,416 FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998
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STREET: 90:
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901 California Avenue
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; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3
; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-215-211-6
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TITLE OF INVENTION: INTERLEUKIN-1 RECEPTORS IN

FILE REFERENCE: 3321-A

CURRENT APPLICATION NUMBER: US/10/215,211

CURRENT FILING DATE: 2002-08-07

PRIOR APPLICATION NUMBER: US 60/310,789

PRIOR FILING DATE: 2001-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sims, John APPLICANT: Smith, Dir
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                SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVE 359
                                                                                  VPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE 300
                                                                                                                                                      CYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTEHLTRTLTVKVVGSFKNA 240
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                                                                                                                                      CYKIQNFNNVI PEGMNLSFLI ALI SNNGNYTCVVTY PENGRTFHLTRTLTVKVVGSPKNA
                                                                                                                                                                                                                        YCSKVAFPLEVVQKDSCFNSPMKLFVHKLYIEYGIQRITCPNVDGYFPSSVKFTITWYMG 180
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SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVTQKVPAPRYTVE
                                                                  VPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE
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llarity 99.7%;
Conservative
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Pred. No. 7.6e-148;
D; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE TREATMENT OF DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 359;
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 359
                                                                    300
                                                                                                                                      240
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RESULT 5 US-09-935-868-28 ; Sequence 28, Application US/09935868 ; Patent No. US20020164690A1

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US-10-011-548-4
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SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/10011548 Publication No. US20030055218A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US99/22045
PRIOR FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/935,868
CURRENT FILING DATE: 2002-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Regeneron Pharmaceuticals, Inc
TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and
FILE REFERENCE: REG 203D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 910
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSES: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,548
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTILLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST
                                                                                                                                                                                                                                                                                                                                                                             TITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLADSRNEVAWTIDGKKPDDITIDVTINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTV 358
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                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                      Bazan, J. Pernando
Kastelein, Robert A.
INVENTION: Human Receptor Proteins; Related Reagents and
                                                                                                                                                                94304-1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Timans, Jacqueline C. Debets, Johannes Eduard
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sana, Theodore R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antonius
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                                                                                                                                                                                                                                                                                                                                                     Methods
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  US/10/011,548
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Pred. No. 6.3e-147;
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                                                Version
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                     453 AVFDFIQRSRRMIVVLSPDYVTEKSISMLEFKLGVMCQNSIAT---KLIVVEYRPLEHPH 509
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459 DLTRYVEQSRRLIIVLTPDYILRRGWSI--FELESRLHNMLVSGEIKVILIECTELK--- 513
                                                                                                                                                                                                               340
                                                                                                                                                                                                                                                                                                         287
                                                                                                                                                                                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 TYCSKVAFPLEVVQKDS--CFNSPMKLPVHKLYIEYG----IQRITCPNVDGYFPSSVKP 173
                                                                                                                  399
                                                                                                                                                              402 GKEYDIYVSYAR------NAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVE 452
                                                                                                                                                                                                                                                                                                                                                                                                232 TALLTDKPPKPLFPMENQPSVIDVQLGKPLNIPCKAFFGFSGESGPMIYW-MKGEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                            234 VGSPKNAVP-PVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKADDI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MTLLWC-VVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVVWYKECKPKMWRSIIIQKGNALLIQEVQEEDGGNYTCELKY--EGKL--VRRTTELKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKV 233
                                                                                                                                                                                                                                                 AKAAKVKQKVPAPRYTVELACGFGATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILD
                                                                                                                                                                                                                                                                                                                                                  TIDVTINESISHSRTEDETR------TQILSIKKVTSEDLKRSYVCHARSAKGEV 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LALVVCSVVSTNLKMVSKRNSVDGCIDWSVD-LKTYMALAGBPVRVKCALFYSYIRTNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAQSTGLRLMWY--KNKGDLEEPIIF--SEVRMSKEEDSIWFHSAEAQDSGFYTCVLRNS 121
                                                                                                                    NKEYDAYLSYTKVDQDTLDCDNPEEEQFALEVLPDVLEKHYGYKLFI PERDLI PSGTYMB
                                                                                                                                                                                                            - KHASVLLRKKDLIYKIELAGGLGAIFLLLVLLVVIYKCYNIELMLFYRQHFGADETNDD
                                                                                                                                                                                                                                                                                                      ----FIEELAGHIR-EGEIRLLKEHLGEKEVELALIFDSVVEADL-ANYTCHVENRNGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYCMKVSMSLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCPDMDDFKKSDQEP 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60
FILING DATE: 15-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/173,151
FILING DATE: «Unknown»
APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-MOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
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Pred. No. 4.9e-58;
Nismatches 244
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Gaps

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458

398 401 339 286

231

Length 686; Indels 136;

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RESULT 6

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Best Local Similarity

35.1%;

Score 800; DB 9

DB 9;

Length 579

Query Match

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RESULT 7
US-10-011-548-2
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US-10-011-548-2
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Publication No. US20030055218A1
                                                                                                                                        INFORMATION FOR SEQ ID NO: 2:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                            NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0767X
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (650)852-9196
                     SEQUENCE DESCRIPTION: SEQ ID NO:
                                     MOLECULE
                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/011,548 FILING DATE: 22-Oct-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                    FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
                                                        TOPOLOGY: linear
                                                                                                LENGTH: 579 amino acids
                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/078,416
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/095,987 FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DNAX Research Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/173,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICATION NUMBER: US 60/081,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILING DATE: <Unknown>
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Kastelein, Robert A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35, Application No. US2003 GENERAL INFORMATION:
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         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHPG---
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                                                                                                                                                                    STREET: 901 California Avenue
CITY: Palo Alto
                                                                                                                                                  STATE: California
                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                          ADDRESSEE: DNAX Research Institute
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Debets, Johannes Eduard Maria
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Kastelein, Robert
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                   Version #1.30
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                342
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mes 204; Conserv
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                    VLLTLRGVLENEFGYXLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEXSISM 480
                                                                                                                                                          LIVCLVTIYKCYKIBIMLFYRNHFGAEELDGDNKDYDAYLSYTKVDPDQWNQETGEEERF 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFRLPENRISKEKDYLWFRPTILADTGNYTCMLRNTTYCSKVAFPLEVVQKDS--CFNSP 141
                                    LEFKLGVMCQNSIAT---KLIVVEYRPLEHPHPGILQLKE-----SVSFVSWKGEK 528
                                                                                                                                                                                                   LVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYAR-----NAEEEEF 420
                                                                                                                                                                                                                                                                                  ETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELACGFGATVL 369
                                                                                                                                                                                                                                                                                                                                                                    KEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDI-----TIDVTINESISHSRTED 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKLPVHKLYIEYG----IQRITCPNVDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF--DGŚRMSKEEDSIWFRPTLLQDSGLYACVIRNSTYCMKVSISLTVGENDTGLCYNSK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTDWSID-IKKYQVLVGEPVRIKCALFYGYIRTNYSLAQSAGLSLMWYKSSGPGDFEEPI
                                                                                                                                                                                                                                              EVSISLI-VDSVEEGDL-GNYSCYVENGNGR--RHASVLLHKRELMYTVELAGGLGAILL
                                                                                                                                                                                                                                                                                                                           TOLGDSANLTCRAFFGYSGDVSPLIYWMKGEKFIEDLDENRVWESDIRI---LKEHLGEQ 285
                                                                               ALEILPDMLEKHYGYKLFIPDRDLIPTGTYIEDVARCVDQSKRLIIVMTPNYVVRRGWSI 461
FELETRLRNMLVTGEIKVILIECSELR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650)852-9196
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APPLICATION NUMBER: US 60/078,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/078,008
FILING DATE: 12-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/081,883 TILING DATE: 15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/173,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---YFEKAELSKSKEISCRDIEDFLLPTREPEILWYKECRTKTWRPSIVFKRDTL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 5.2e-53;
9; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DX0767X
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GIMNYQEVEALKHTIKLLTVIKWHGPK
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Publication No. US20030055218A1
GENERAL INFORMATION:
                                                                                                           INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 SKHSGSKFWKALRLALPLR---
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/062,066 FILING DATE: 15-OCT-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins;
                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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MOLECULE TYPE:
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                     STRANDEDNESS: No. US20030055218A1 Relevant TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/011,548 FILING DATE: 22-Oct-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                         NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
                                                                 TYPE: amino acid
                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
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APPLICATION NUMBER: US 60/065,776
FILING DATE: 17-NOV-1997
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CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/078,008 FILING DATE: 12-MAR-1998
                                                                                           LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/078,416
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Debets, Johannes Eduard Maria
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                                                                                        541 amino acids
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Query Match
Best Local Similarity 30...
174; Conservative
                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09981421 Patent No. US20020098185A1 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                        SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 174;
                                                                                                                                                                   FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 60/241,408
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                            APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall
APPLICANT: Born, Teresa L.
                                                                                                                                                        SOFTWARE: PatentIn
                                                                                          ORGANISM: Homo sapiens
                                                                                                            TYPE: PRT
                                                                                                                                                                                                                                                              PPLICANT: Born, Teresa L.
ITLE OF INVENTION: METHODS FOR TREATING IL-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEIETTTKSWYKSSGSQEHVE-LNPR-SSSRIALHDCVLEFWPVELNDTGSYFFQMKNYT 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIRSLIEKSRRLIIVLSKSYMSNEVRYELESGLHEALVERKI--KIILIEFTPVTDFTFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q----KWKLNVIRRNKHSCFTERQVTSKIVEVKKFF-----QITCEN--SYYQTLVNST 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSAGLTL-IWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTT 120
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                                                                                                                         541
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                                                                                                                                                         version 3.1
                                                                                                                                                                                                                                                                                           Kendall M.
              14.4%; Score 528; DB 10; 30.0%; Pred. No. 3e-34; tive 93; Mismatches 215;
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Pred. No. 3e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215; Indels
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                                           Length 541;
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                98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/10157447 Patent No. US20020143155A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486
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                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                       CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated
                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWVLISV---
                                                                                                                                                                                                                                                                              STATE: WA
COUNTRY: USA
                                                        APPLICATION NUMBER: 09/110,618
                                                                        APPLICATION NUMBER: US/09/578,178
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                   ZIP: 98101
                                                                                                                                                                                                                                                                                                              CITY: Seattle
                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Kathryn A. STREET: 51 University
                                              FILING DATE:
              Anderson,
                                              <Unknown>
            Kathryn A.
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Immunex Corporation

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312 ILVRKADMADIPGHVFT----RGMIIAVLILVAVVCLVTVCVIYRVDLVLFYRHLTRRDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YCSKVAFPLEVVQ--KDSCFN----SPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPT
                                                                                                           EIHSLIEKSRRLIIVLSKSYMSNEVRYELESGLHEALVERKI--KIILIEFTPVTDFTFL
                                                                                                                                                                                                                                                       TILDGKEYDIYVSYAR-----NABEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVE
                                                                                                                                                                                                                                                                                                                                                                      HSAGLTL-IWYWTRODRDLEBPINFRLPENRISKEKDYLWFRPTLLNDTGNYTCMLRNTT 120
                                              PGILOLKESVSFVSWKGEKSKHSGSKFWKALRLALPLRSL 549
                                                                                                                                                                AVFDFIQRSRRMIVVLSPDYVTEKSISMLEFKL-GVMCQNSIATKLIVVEYRPLEHPH--
                                                                                                                                                                                                                       TLTDGKTYDAFVSYLKECRPENGBEHTFAVEILPRVLEKHFGYKLCIFERDVVPGGAVVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGSPKNAVPPV1HSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDIT
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POSLKILKSHRVLKWKADKSLSYNSRFWKNILLYLMPAKTV 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDVTINESISHSRTEDETRT-----QILSIKKVTSEDLKRSYVCHARSAKGEVAKAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEIETTTKSWYKSSGSQEHVE-LNPR-SSSRIALHDCVLEFWPVELNDTGSYFFQMKNYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -HEEKEMRIMTPEGKWHASKVLRIENIGESNLNVLYNCTVASTGGTDTKSF
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US-10-011-548-32
                                                                                                                                                                                                  Sequence 32, Application US/10011548 Publication No. US20030055218A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 174;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 453 AVFDFIQRSRRMIVVLSPDYVTEKSISMLEFKL-GVMCQNSIATKLIVVEYRPLEHPH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      398 TILDGKEYDIYVSYAR-----NAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVE 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 HSAGLTL-IWYWTRQDRDLEEPINFRLPENRISKEKDYLWFRPTLLNDTGNYTCMLRNTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LWCVVSLYFYGILQSDASERCDDWGLDTMR-QIQVFEDBPARIK-CPLFEHFLKFNYSTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                          TITLE OF
                                                                                                                                               APPLICANT: Timans, Jacqueline C.
Debets, Johannes Eduard Maria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q----KWKLNVIRRNKHSCFTERQVTSKIVEVKKFF-----QITCEN--SYYQTLVNST 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVKQK-----VPAPRYTVELACGFGATVLL---VVILIVVYHVYMLEMVLFYRAHFGTDE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCSKVAFPLEVVQ--KDSCFN----SPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPT 174
                                                                                                                                                                                                                                                                                                                                                                                 POSLKLLKSHRVLKWKADKSLSYNSRFWKNLLYLMPAKTV 525
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SLYKNCKKLLLENNKNPTIKKNAEF-----EDQGYYSCVHFLHHNGKLFNITKTFNITI 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                 PGILQLKESVSFVSWKGEKSKHSGSKFWKALRLALPLRSL 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLTDGKTYDAFVSYLKECRPENGEEHTFAVEILPRVLEKHFGYKLCIFERDVVPGGAVVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDVTINESISHSRTEDETRT-----QILSIKKVTSEDLKRSYVCHARSAKGEVAKAA 345
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REFERENCE/DOCKET NUMBER: 261
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                     Bazan, J. Fernando
Kastelein, Robert A.
INVENTION: Human Receptor Proteins; Related
                                                                                               Sana, Theodore R.
                                                                                                                       Antonius
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30.0%; Pred. No. 3e-34;
vative 93; Mismatches 2
Methods
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                       Reagents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 32:
                                                                                                                          168
                                                                                                                                                                          183
                          228 MRPEFIY-PNNNTI-EVELGSHVVMECNVSSGVYGLL-
                                                                                                                                                                                                                                                                         126 AFPLEVVQKDS--CFNSPMKLPVHKLYIEYGIQRITCPNVDGY-FPSSVKPTITWYMGCY 182
                                                                                                                                                                                                                                                                                                                               55
                                                                                                                                                                                                                                                                                                                                                                            66 LTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKV 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 555 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030055218A1 Relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-MAR-1998
APPLICATION NUMBER: US 60/062,066
FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/011,548
FILING DATE: 22-Oct-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 36
                                                                     AVPPVIHSPNDHVVYEKEPGEELLIPCTV---YFSFLMDSRNEVWWTIDGKKPDDITIDV 296
                                                                                                                       SGFLEDKRLVLAEGENAILILNVTIODKGNYTCRMVYTYMGKQYNVSRTMNLEVKESPLK 227
                                                                                                                                                                       K--IQNFNNVIPEGMN-LSPLIALISNNGNYTCVVTYPENGRTPHLTRTLTVKVVGSPKN 239
                                                                                                                                                                                                                            IINLKVFKNDNGLCFNGEMK--YDQIVKSANAGKIICPDLENFKDEDNINPEIHWYKBCK 167
                                                                                                                                                                                                                                                                                                                               YNLTWY--RNGSNM--PITTE-RRARIHQRKGLLWFIPAALEDSGLYECEVRSLNRSKQK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                 CVICNYF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650)496-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
APPLICATION NUMBER: US 60/078,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/078,008 FILING DATE: 12-MAR-1998 APPLICATION NUMBER: US 60/081,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/065,776 FILING DATE: 17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 09/173,151
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ilarity 26.4%;
Conservative 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 496; DB 9;
Pred. No. 1.2e-31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30, Application US/10011548 Publication No. US20030055218A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 QLKESVSFVSWKG---EKSKHSGSKFWKALRLALPLRSLSASSGWNES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/10/011,548
FILING DATE: 22-OCT-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                   REFERENCE/DOCKET NUMBER: DX0767X TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .TYREQFYEEGMPHGIAVSGTK---FNISEVKLKDYAYKFFCHFIYDSQEFTSYIKLEH--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IVVLSP-----DYVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLE---HPHPGIL 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAPRYTVELACGFGATVLLVVILIVVYHVYWLEMVLFYRA--HFGTDETILDGKEYDIYV
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CITY: Palo Alto
STATE: California
                                                                            NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                             APPLICATION NUMBER: US 60/062,066 FILING DATE: 15-OCT-1997
                                                                                                                                                                                       APPLICATION NUMBER: US 60/078,416 FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                  FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/173,151 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94304-1104
                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                       FILING DATE: 12-MAR-1998
                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/065,776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/081,883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF INVENTION: Human Receptor Proteins; Related Reagents
Methods
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Debets, Johannes Eduard Maria
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Kastelein, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sana, Theodore R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antonius
(650) 496-1200
                    (650) 852-9196
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RESULT 14
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                                                                                                                                                                                                             Sequence 4, Application US/09731175
Patent No. US20020098168A1
GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                                                                                                                                            522
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                                                                                                                APPLICANT: Grorioso, Joseph C.
APPLICANT: Grorioso, Joseph C.
Evans, Christopher H.
Robbins, Paul D.
Robbins, Paul D.
TITLE OF INVENTION: Gene Transfer for Studying and Treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPD------
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                                                                                                                                                                                                                                                                                                                                            FQERPQSAKTRFWKNLRYQMPAQRRS-----PLSKHRLLTLDPVRDTKEKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTATIVCCVCIYKVFKVDIVLWYRDSCSGFLPSKASDGKTYDAYILYPKTLGEGSFSDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVLLVVILIVVYHVYWLEMVLFYRAHFG--TDETILDGKEYDIYVSYARNAEE-----E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRKYTLITTINISEVKSQFYRYPFICVVKNT--NIFESAHVQLIYPVPDFKNYLIGGFII 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADPGSMIQLICNVTGQF----SDLVYWKWNGS-----BIEWNDPFLAEDYQFVEHPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFLIALIS--NNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPMKLPVHKLYIEYGIQRITCPNVDGYF--PSSVKPTITWYMGCYKIQNFNNVIPEGMNL 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIDVCTEYPNQIVLFLSVNEIDIRKCPLTPNKMH-----GDTIIWY----KNDSKT 67
                                                                                                                                                                                                                                                                                                                                                                              --EKSKHSGSKFWKALRLALPLRSLSASSGWNESCSSQSDISLDHVQRRRSRL
                                                                                                                                                                                                                                                                                                                                                                                                               GQSSEEQIAI----YNALIQEGI--KIVLLELBKIQDYEKMPDSIQFIKQKHGVICWSGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     -YVTEKSISMLBFKLGVMCQNSIATKLIVVEYRPLE--HPHPGILQ-LKESVSFVSWKG- 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TFVFKLLPEVLEGQFGYKLFIYGRDDYVGEDTIEVTNENVKKSRRLIIILVRDMGGFSWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDE-TRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELACGFGA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEPGEELLIPCTVYFSPLMDSRNEVWWTIDGKKPDDITIDVTINES-----ISHSRT 307
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153; Conser
STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: No. US20030055218A1 Relevant TOPOLOGY: linear
                                                  ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                 CITY: San Francisco
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Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCPLFEHFLKFNYSTAHSAGLTLIWYWTRODRDLEE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.1e-30;
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ZIP: 94111-3834

CURRENT APPLICATION DATA:

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,

Version #1.30

Ploppy disk

APPLICATION NUMBER: US/09/731,175 FILING DATE: 05-Dec-2000

CLASSIFICATION:

<Unknown>

COMPUTER READABLE FORM:

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Gaps
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JS-10-011-548-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                              INFORMATION FOR SEQ ID NO: 29: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 FQERPQSAKTRFWKNLRYQMPAQRRS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bazan, J. Fernando
Kastelein, Robert A.
TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and
               MOLECULE TYPE: peptide SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/011,548 FILING DATE: 22-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: <Unknown>
                                                                        TYPE: amino acid
STRANDEDNESS: No. US20030055218A1 Relevant
                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 901 California
CITY: Palo Alto
                                                             TOPOLOGY: linear
                                                                                                                            LENGTH: 537 amino acids
                                                                                                                                                                                            TELEFAX:
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                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                  NAME: Ching,
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/078,416 FILING DATE: 18-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/173,151 FILING DATE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/062,066 FILING DATE: 15-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-NOV-1997
APPLICATION NUMBER: US 60/078,008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Timans, Jacqueline C.
Debets, Johannes Eduard Maria
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                                                                                                                                                                                            (650)496-1200
                                                                                                                                                                                                                (650) 852-9196
                                                                                                                                                                                                                                                                                                      Edwin P.
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                    SEQ ID NO: 29:
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US-09-731-175-4 Matches 153; Conservative 120; Mismatches Best Local Similarity Query Match INFORMATION FOR SEQ ID NO: 4: 127 TOATFP-ORLHIA-GDGSLVCPYV-SYFKDENNELPEVOWYKNC-KPLLLDNVSFFGVKD 182 348 LTATIVCCVCIYKVFKVDIVLWYRDSCSGPLPSKASDGKTYDAYILYPKTLGEGSFSDLD 407 290 KRKYTLITTLNISEVKSQFYRYPFICVVKNT--NIFESAHVQLIYPVPDPKNYLIGGFII 347 308 EDE-TRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELACGFGA 366 241 256 KEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINES-----ISHSRT 307 183 KLLVRNVAEEHRGDYICRMSYTFRGKQYPVTRVIQFITIDENKRD-RPVILSPRNETI-E 240 198 SFLIALIS--NNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYB 255 140 SPMKLPVHKLYIEYGIQRITCPNVDGYF--PSSVKPTITWYMGCYKIQNFNNVIPEGMNL 197 419 EFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPD 8 82 PINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDS--CFN 139 21 EIDVCTEYPNQIVLFLSVNEIDIRKCPLTPNKMH------GDTIIWY----KNDSKT 67 34 QIQVFEDEPARI------KCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEE 81 SEQUENCE DESCRIPTION: SEQ ID NO: 4: TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE CHARACTERISTICS: LENGTH: 576 amino acids TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200 ATTORNEY/AGENT INFORMATION: PRIOR APPLICATION DATA: ADPGSMIQLICNVTGQF----SDLVYWKWNGS-----EIEWNDPFLAEDYQFVEHPST 289 PISAD-RDSRIHQQNEHLWFVPAKVEDSGYYYCIVRNSTYCLKTKVTVTVLENDPGLCYS 126 TVLLVVILIVVYHVYWLEMVLFYRAHFG--TDETILDGKEYDIYVSYARNAEE-----E 418 NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 018484-002280US APPLICATION NUMBER: 08/924,777 FILING DATE: 2000-01-31 TYPE: amino acid TELEFAX: (415) APPLICATION NUMBER: US 08/685,212 APPLICATION NUMBER: US 08/567,710 FILING DATE: 05-DEC-1995 APPLICATION NUMBER: US 07/963,928 FILING DATE: 20-OCT-1992 FILING DATE: 23-JUL-1996 APPLICATION NUMBER: US 08/027,750 FILING DATE: 08-MAR-1993 LING DATE: 18-JAN-1994
PLICATION NUMBER: US 08/381,603
LING DATE: 27-JAN-1995 PLICATION NUMBER: US 08/183,563 13.2**%**; 25.8**%**; 576-0300 Score 484.5; DB 1 Pred. No. 1.1e-30; DB 10; Length 576; 225; Indels 95;

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                                                                                                                                                             500 VEYRPLEHPH--PGILQLKESVSFVSWKGEKSKHSGSKFWKALRLALPLRSLSASSGWNE 557
                                                                                                                                                                                                                       558 SCSSQSDIS 566
                                                                                                                 471 IEFTPASNITFLPPSLKLLKSYRVLKWRAD-SPSMNSRFWKNLVYLMPAKAVKP----WRE 526
                                                                                                                                                                                                                                                                                                                                      353 VLFYRRIAERDETLTDGKTYDAFVSYLKECHPENKEEYTFAVETLPRVLEKQFGYKLCIF 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 TKTVNITVI-EGRSKVTBAILGPKCEKV-GVELGKDVELNC----SASLNKDDLFYWSI- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 TRTLTVKVVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLADSRNEVWWTID 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 VGN----DRRNWTLNVTKRNKHSCFSD------KLVTSRDVEVNKSLHITCKNPNYEEL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 LRWTTYCSKVAFPLEVVQ--KDSCFNSPMKLPVHKLYIEYGIQ-----RITC--PNVDGY 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         338 KGEVAKAAKVKOK----VPAPRYTVELACGFGATVLL-----VVILIVVYHVYWLEM 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 IQD-----TWLYKNCKEISKTPRILKD-----AEFGDEGYYSCVFSVHHNGTRYNI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 GKKPDDITIDVTINESISHSRTEDET-----RTQILSIKKVTSEDLKRSYVCHARSA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167 PPSSVKPTITW-YMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ---ETA----TMRWFKGSASHEYRELINIRSSP--RVTFHDHTLEFWPVEMEDEGTYISQ 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 FNYSTAHSAGLTLIWYWTRODRDLEBPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIK-----CPLFEHFLK 55
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ESEARSVLS 535
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Search completed: April 23, 2003, 09:00:26 Job time : 4 $\beta$  secs

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Result
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Maximum Match 100%
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Maximum DB
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Perfect score:
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3669
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  GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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ST2 protein - huma
Fit-1S protein pre
B15R protein precu
interleukin-1 beta
                                        Toll protein precu
MyD88 protein - mo
neural cell adhesi
Toll protein-like
cell adhesion mole
                                                                                             B16R protein - vac
ST2V protein - hum
type I interleukin
           Bravo/Nr-CAM cell
protein UNC-89
                               cell adhesion mole
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Fit-1M protein - r
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 cell adhesion
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interleukin-1 rece
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interleukin-1 rece
lymphocyte antigen
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elastic titin - hu
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## ALIGNMENTS

RESULT 1
A57535
(;Species: Mus musculus (house mouse)
(;Species: Mus musculus (house mouse)
(;Species: Mus musculus (house mouse)
(;Date: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 17-Mar-2000
(;Cate: 08-Feb-1996 #sequence\_revision 08-Feb-1996 #text\_change 17-Mar-2000
(;Accession: A57535
R,Greenfeder, S.A.; Nunes, P.; Kwee, L.; Labow, M.; Chizzonite, R.A.; Ju, G.
J. Biol. Chem. 270, 13757-13765, 1995
A;Title: Molecular cloning and characterization o a second subunit of the interleuki A;Reference number: A57535; MUID:95293970; PMID:7775431
A;Accession: A57535

A;Molecule type: mRNA A;Residues: 1-570 <GRE> A;Residues: 1-570 <GRESA A;Cross-references: GB:X85999; NID:g887520; PIDN:CAA59991.1; PID:g887521 C;Superfamily: interleukin-1 receptor type I C;Keywords: transmembrane protein

A; Status: preliminary

	(D (D )	O E B !		<b></b>			י טיס מ	
Ş	92 93	8 . <b>Q</b>	B 8	B 8	Db Qq	Db Q7	B &	Que Mat
421 VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISM 480	361 ACGFGATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEEF 420 	301 SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKOKVPAPRYTVEL 360  : :	241 VPPVIHSDNDHVVYEKEPGEELLIPCTVYPSPLMDSRNEVWWTIDGKKPDDITIDVTINE 300     -	181 CYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNA 240   :  :  :  :	121 YCSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMG 180	61 AHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLINDTGNYTCMLRNTT 120    :	1 MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST 60           :	Query Match 63.4%; Score 2327.5; DB 2; Length 570; Best Local Similarity 75.9%; Pred. No. 4.4e-168; Matches 429; Conservative 66; Mismatches 55; Indels 15; Gaps 5;

554

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interleukin-1 receptor I precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992
C;Accession: JQ1526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 111, 239-243, 1992
A;Title: The chicken IL-1 receptor: differential evolution of the A;Reference number: JQ1526; MUID:92175529; PMID:1531799
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R;Guida, S.; Heguy, A.; Melli, M.
Gene 111, 239-243, 1992
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;Keywords: cytokine receptor; transmembrane protein
;I-19/Domain: signal sequence #status predicted <SIG>
;10-555/Product: interleukin-1 receptor I #status predicted
;339-359/Domain: transmembrane #status predicted <TRA>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKFWKALRLALPLRSLSASSGWNES 558
                                                                                                                                                                                                                                                                                                 MRPEFIX-PNNNTI-EVELGSHVVMECNVSSGVYGLL-----PYHQVNDEDVD--SFDS
                                                                                                                                                                                                                                                                                                                                AVPPVIHSPNDHVVYEKEPGEELLIPCTV---YFSFLMDSRNEVWWTIDGKKPDDITIDV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                   IINLKVFKNDNGLCFNGEMK--YDQIVKSANAGKIICPDLENFKDEDNINPEIHWYKECK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFPLEVVQKDS--CFNSPMKLPVHKLYIEYGIQRITCPNVDGY-FPSSVKPTITWYMGCY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLINDTGNYTCMLRNTTYCSKV 129
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                                                                                                 LYPKNRESCLYSSDIFALKILPEVLERQCGYNLFIFGRNDLAGEAVIDVTDEKIHQSRRV
                                                                                                                                                                                                                                                                                                                                                                SGFLEDKRLVLAEGENAILILNVTIQDKGNYTCRMVYTYMGKQYNVSRTMNLEVKESPLK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YNLTWY--RNGSNM--PITTE-RRARİHQRKGLLWFIPAALEDSGLYECEVRSLNRSKQK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LELKAGL---ENMASRGNINVILVQYKAVKDMK--VKELKRAKTVLTVIKWKGEKSKYPQ 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLLTLRGVLENEFGYKLCIFDRDSLPGGIVTDETLSFIQKSRRLLVVLSPNYVLQGTQAL
QLKESVSFVSWKG---EKSKHSGSKFWKALRLALPLRSLSASSGWNES
                                IIILVPEPSCYGILEDASEKHLAV----YNALIQDGI--KIILIELEKIEDYANMPESIK
                                                                                                                           SYARNAB-----EEEFVLLTLRGVLENEFGYKLCIFDRDSLFGGNTVEAVFDFIQRSRRM 464
                                                                                                                                                                 PVQNIRGYLIGGGISLIFLLFLILIVYKIFKIDIVLWYRSSCHPLLGKKVSDGKIYDAYV
                                                                                                                                                                                                PAPRYTVELACGFGATVLLVVILIVVYHVYWLEMVLFYRA--HFGTDETILDGKEYDIYV
                                                                                                                                                                                                                                 TYREOFYEEGMPHGIAVSGTK---FNISEVKLKDYAYKFFCHFIYDSQEFTSYIKLEH--
                                                                                                                                                                                                                                                  T----INESISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKV 351
                                                                 IWLSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                              -DYVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLE---HPHPGIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.5%; Score 496; DB 2; Length 555, 26.4%; Pred. No. 1.7e-29; Vative 109; Mismatches 230; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -VLVGEPTAISCPV-----ITLPMLHS-D 54
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558
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interleukin-1 receptor precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990
C;Accession: A32604
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interleukin 1 receptor type I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-590 <RES>
A;Cross-references: GB:M95578; NID:g451305; PIDN:AAA16196.1;
C;Superfamily: interleukin-1 receptor type I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Neuroimmunol. 44, 49-56, 1993
A;Title: An mRNA homologous to interleukin-1 receptor type I
A;Reference number: I56526; MUID:93266794; PMID:7684399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: I56526
A; Status: preliminary; translated
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R;Hart, R.P.; Liu, C.; Shadiack, A.M.; McCormack, R.J.; Jonakait,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 TYGKQYPVTRVITFITIDDSKRD-RPVIMSPRNETM-EADPGSTIQLICNVTGQF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 NDTGNYTCMLRNTTYCSKVAFFLEVVQKDS--CFNSPMKLPVHKLYIEYGIQRITCPNVD 164
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                                                     RSLSASSGWNESCSSQSDISLDHVQRRRSRLKEPPEL 583
                                                                                                                                                              LIVVEYRPLEHPHPGILQLKESVSFVS-----WKG---EKSKHSGSKFWKALRLALPL 546
                                                                                                                                                                                                                    GEDTIEVTNENVKRSRRLIIILVRD------MGSFSCLGQSSEEQIAIYDALIREGIK
                                                                                                                                                                                                                                                                       GGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISMLEFK-LGVMCQNSIA-----TK 496
                                                                                                                                                                                                                                                                                                                             DFLPRKASDGRTYDAYVLYPKTYGEGSFAYLDTFVFKLLPEVLEGQFGYKLFICGRDDYV 449
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                                                                                                           IILLELEKIODYE----KMPESIQFIKQKHGAICWSGDFKERPQSAKTRFWKNLRYQMPA
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PLSKHHLLTLDPVLDTKEKLQAETHL
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Pred. No. 2.9e-29;
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     . 587
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29-Sep-1999

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A;Cross-reterences. C., A;Cross-reterences. C., A;Cross-reterences. C., Superfamily: interleukin-1 receptor; phosphoprotein C;Keywords: cytokine receptor; glycoprotein; phosphoprotein C;Keywords: cytokine receptor; glycoproteid cytokin-1 receptor #status predicted F;10-576/Product: interleukin-1 receptor #status predicted F;30-579/Domain: transmembrane #status predicted cytokin-1 receptor #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,145-199,251-315/Disulfide bonds: #status predicted F;46-99,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,461-499,499,499,499,499,499,499
C;ACCEBBANA, K.; Takagi, T.; LEUNAMINE, R;Yanagisawa, K.; Takagi, T.; LEUNAMINE, R;Yanagisawa, K.; Takagi, T.; LEUNAMINE, SB, LETT. 318, 83-87, 1993
A;Title: Presence of a novel primary response A;Title: Presence of a novel primary response PMI
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A;Accession: A32604
A;Accession: MEMA
A;Residues: 1-576 <SIM>
A;Cross-references: GB:M20658; GB:M29752; NID:g198300; PIDN:AAA39279.1;
                                                                                                                                                                                         lymphocyte antigen Ly84 precursor - mouse N;Alternate names: 38.5K T1 glycoprotein; ST2L protein C;Species: Mus musculus (house mouse)
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Pred. No. 1.4e-28;
0; Mismatches 225;
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PMID:7916701
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FEBS Lett. 258, 301-304, 1989
A;Title: A putative protein of a growth specific cDNA from A;Title: A putative protein of a growth specific cDNA from A;Teference number: S07054; MUID:90092495; PMID:2532153
A;Accession: S07054
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A;Residues: 1-191,'V',193-328,'SKECPSHIA' <KLE>
A;Cross-references: GB:M24843; NID:9201103; PIDN:AAA40160.1; PID:9201104
A;Crominaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka, Biochim: Biophys. Acta 1090, 1-8, 1991
A;Title: Molecular cloning of the murine ST2 gene. Characterization and A;Reference number: S17657; MUID:91355215; PMID:1832015
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Proc. Natl. Acad. Sci. U.S.A. 86, 5708-5712, 1989
A;Title: Serum- and oncoprotein-mediated induction of a A;Reference number: A33541; MUID:89345336; PMID:2527364
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-567 < YAN>
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F;60,101,107,146,176,194,225,259,278/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-26/Domain: signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 1
A; Introns: 27/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-328,'SKECPSHIA' <TO2>
A;Residues: 1-328,'SKECPSHIA' <TO2>
A;Cross-references: EMBL;Y07519; NID:g55517; PIDN:CAA68812.1;
A;Note: it is uncertain whether Met-1, Met-7 or Met-19 is the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-191,'V',193-328,'SKECPSHIA' <TOM>
A;Cross-references: EMBL:X60184; NID:g54200; PI
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Best Local
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                                                   LEYDCLALNLHGMIRHTIRLRRKQPIDHRSIYYIVAGCSLLLMFINVLVIVLKVFWIEVA
                                                                                                                                                                                                                                                                                        LW--CVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTA
                                                                                                             RSYVCHARSAKGEVAKAAKVKQKVPAPRYTV-BLACGFGATVLLVVILIVVYHVYWLEMV
                                                                                                                                                                                                                              VWWTIDGKKPDDITIDVTINESISHSRTEDE-----TRTQILSIKKVTSEDLK 327
                                                                                                                                                                                                                                                                                                                                              HLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFS----FLMDSRNE
                                                                                                                                                                                                                                                                                                                                                                                                           VQWFKNCKALQEPRFRAHRSYLFIDNVTHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITWYMGCYKIQN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKTGYLNVTIHKKPPSCNIPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YPVEWYYS----DTNESIPTQ-KRURIFVSRDRLKFLPARVEDSGIYACVIRSPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSAGLTLIWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LWALAILTLPMY-LTVTEGSK--SSWGL
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                                                                                                                                                                       -QINKTVVGNFGEARIQEEEGRNESSSNDMDCLTSVLRITGVTEKDLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 478; DB 2;
Pred. No. 4.1e-28;
D5; Mismatches 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -YLMYSTVRGSDKNFKITCPTIDLY---NWTAP 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN: CAA42742.1;
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                                                                                                                                                                                                                                                                                                                                                                                                        -DEGDYTCQFTHAENGTNY
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BALB/c-3T3

cells

3.

PID:954201

and chromosomal

initiator PID:955518

134;

Gaps

28;

49 61

386

303

198

279

253

174 100 (Asn)

(covalent)

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511

GILQLKESVSFVSWKG---EKSKHSGSKFWKALRLALPLR

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RESULT
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A;Residues: 1-562 <LOV>
A;Cross-references: EMBL:U49065; NID:g1236078; PIDN:AAB53237.1;
C;Superfamily: interleukin-1 receptor type I
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A;Accession: G02426
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Matches 148;
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                                                                                                                                                                                                                               273 YYDESKRIREGVETHVSFREHNLYTVNITFLEVKMEDYGLPFMCHAG-----VSTAYII 326
                                                                                                                                                                                                                                                                                                                                                                                         160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103
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                                                                                                                                                                                                                                                                                                                                              234 V--GSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDD 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 TILWCVVSLYFYGILQSDASERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYSTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LFWRDIVTPYKTRNDGKLYDAYIIYPRVFRGSAAGTHSVEYFVHHTLPDVLENKCGYKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LALPL-RSLSASSGWNESCSSQSDISLDH 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SKVILIEMEPLGEASRLQVGDLQDSLQHLVKIQGTIKWREDHVADKQSLSSKFWKHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFYRAHFGTDETILDGKEYDIYVSYAR------NAEBEBEFVLLTLRGVLENEFGYKLC
                                                                                                                                                     LQLPAPDFRAYLIGGLIALVAVAVSVVYIYNIFKIDIVLWYRSAFHSTETIVDGKLYDAY
                                                                                                                                                                         QKVPAPRYTVBLACGFGATVLLVVILIVVYHVYMLEMVLFYRAHFGTDETILDGKEYDIY
                                                                                                                                                                                                                                                                                                                                                                                       KWYKDCNEIKGERFTV---LETRLIVSNVSAEDRGNYACQAILTHSGKQYEVLNGITVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHRIHVNLTVFEKHWCDTSIGGLPNLSDEYKQILHLGKDDSLTC---HLHFPKSCVLGPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSGEVSVTWY----KNSSKIPVS-KIIQSRIHQDETWILFLPMEWGDSGVYQCVIKGRDS 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLLLCGLSI---ALPLSVTADGCKD---IFMKNEILSASQPFAFNC-----TFPPI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YOMPVPERASKTASVAAPLSGKACLDLKH 566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSP-----DYVTEKSISMLEFKLGVMCQNS
RIVIVVPESLGFGLLKNLSEQIAV----YSALIQDGM--KVILIELEKIEDYTVMPE-
                                  RMIVVLSPD-----YVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLEH----PHP
                                                                                                              VSYARNAEEEE-----FVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSR 462
                                                                                                                                                                                                                                                                    ITID-VTINESI-SH-SRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVK 348
                                                                                                                                                                                                                                                                                                          TERAGYGGSVPKIIY-PKNHSI-EVQLGTTLIVDCNV--TDTKDNTNLRCWRVNNTLVDD
                                                                          VLYPKPHKESQRHAVDALVLNILPEVLERQCGYKLFIFGRDEFPGQAVANVIDENVKLCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 119; Mismatches 236;
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C;Accession: A36187; S06928
R;Sims, J.E.; Acres, R.B.; Grubin, C.E.; McMahan, C.J.; Wignall, Proc. Natl. Acad. Sci. U.S.A. 86, 8946-8950, 1989
A;Title: Cloning the interleukin 1 receptor from human T cells.
A;Reference number: A36187; MUID:90046906; PMID:2530587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: 2q12-2q12
C;Superfamily: interleukin-1 receptor type I
C;Keywords: cytokine receptor; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Chua, A.O.; Gubler, U.
Nucleic Acids Res. 17, 10114, 1989
A;Title: Sequence of the cDNA for the human fibroblast type interleukin-1 receptor.
A;Reference number: S06928; MUID:90098789; PMID:2532321
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A;Cross-references: GDB:125254; OMIM:147810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:X16896; NID:g33800; PIDN:CAA34773.1; PID:g33801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-569 < CHU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: S06928
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A; Residues: 1-569 <SIM>
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C;Species: Homo sapiens (man)
C;Species: 14-Dec-1990 #sequence_revision 14-Dec-1990 #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Genetics:
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448
                                                                                 500
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                                                                                                                                                                           331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 MGCYKIQNFNNVIPEGMNLSFLIALIS--NNGNYTCVVTYPENGRTFHLTRTLTVKVVGS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 ISAKFVENEPNLCYNAQAIFKQKLPV-----AGDGGLVCPYME-FFKNENNELPKLQWY 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 11.6%; Score 424.5; Local Similarity 24.3%; Pred. No. 4.6e es 129; Conservative 117; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIQYIKQKHGAIRWHGDFTEQSQCMKTKFWKTVRYHMPPR
                                                                                                                                                                    VTNEQKHM---IGICVTLTVIIVCSVFIYKIFKIDIVLWYRDSCYDFLPIKASDGKTYDA
                                                                                                                                                                                                                                                              VIGEDYYSVENPANKRRSTLITVLNISEIESRFYKHPFTCFAKNTHG--IDAAYIQLIYP
                                                                                                                                                                                                                                                                                                     TINESI----SHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVP 352
                                                                                                                                                                                                                                                                                                                                                  NKPTRPVIVSPANE--TMEVDLGSQIQLICNVTGQL----SDIAYWKWNGSVIDE--DDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FPLEVVQKDS--CFNS----PMKLPVHKLYIEYGIQRITCPNVDGYF--PSSVKPTITWY 178
  RRLIIILVRETSGFSWLGGSSEEQIAM----YNALVODGI--KVVLLELEKIQDYE----
                                             RRMIVVLSPDY --
                                                                                                                                                                                                                      APRYTVELACGFGATVLLVVIL---IVVYHVYWLEMVLFYR--AHFGTDETILDGKEYDI 407
                                                                                                                                                                                                                                                                                                                                                                                          PKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                       KDC-KPLLLDNIHFSGVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEE 220
                                        ---VTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLEHPHPGIL
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                                                                                                                                  461
                                                                                                                                                                             387
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      497
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QLKESVSFVS--

WKGEKS---KHSGSKFWKALRLALPLRSLSASS

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C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 11-Jan-2000
C;Accession: S42633
R;Bergers, G.; Reikerstorfer, A.; Braselmann, S.; Graninger, P.; Busslinger
EMBO J. 13, 1176-1188, 1994
A;Title: Alternative promoter usage of the Fos-responsive gene Fit-1 general
A;Reference number: S42632; MUID:94178260; PMID:8131748
A;Accession: S42633
                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-247 <BEI
                                                                                                                                                                                                                                                                       RESULT 9
$42633
Fit-1M protein - rat
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                                                                 A; Residues: 1-2
C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Bristulf, J.; Gatti, S.; Bartfai, T. submitted to the EMBL Data Library, Way 1993 A;Description: The rat insulinoma beta-cell A;Reference number: $33473 A;Accession: $33473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 receptor type 2 - rat
c;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: $33473
R;Bristulf, J.; Gatti, S.; Bartfai, T.
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Psidues: 1-416 <BRI>
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Best Local S
Matches 97
   Best Loc
Matches
                                    Query Match
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               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFPLVS-YLQISALSSTGLLVCPDLKEFISSRTDGKIQWYKG-
                                                                                                                                                                                                                                                                                                                                                          TFSWGIALAPLSLIILVVGAIWI 381
                                                                                                                                                                                                                                                                                                                                                                                           ACGEGATVLLVVILIVVYHVYWL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHSRTE-DETRTQI-LSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLETI -- PASLGSRLIVPCKVFLGTGTSSNTIVWW-----MANSTFISVAYPRGRVTEGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLSAGDPTRILISNTSMGDAGYYRCVMTFTYEGKEYNITRNIELRVKGITTEPI-PVIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLPVHKLYIEYGIQRIT----CPNVDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNLS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GD----EPRMWVKDDTLWVLPAVQQDSGTYICTFRNASHCEQMSLELKVFK-----NTEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDSCFNSPM 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCWFRGRDFKSELRL-EGEPVVLRCPLVPH-----SDTSSSSRSLL-TWSKSDSSQLIP
                                                                                                                                                                                                                                                                                                                                                                                                                             HHQYSENDENYVEVSLIFDPVTKEDLNTDFKCVATNPRSFQSLHTTVKE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNDHVVYEKEPGEELLIPCTVYFSPLMDSRNEVWWTIDGKKPDDITIDVT----INESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FLIA-----LISUN-----GNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHS
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                 Similarity
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                                                                 interleukin-1 receptor type
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                                                                                    <BER>
                 7.0%;
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; Pred. No. 5.6e-15;
67; Mismatches 153
   45;
                 Score 256;
Pred. No. 8
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   Mismatches
               8e-12;
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                             DB 2;
                                                                                                                                                                                                   S.; Graninger, P.; Busslinger,
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                             Length 247;
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   Indels
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32;
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Gaps
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RESULT 11
S30444
ST2 protein - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_r
C;Accession: S30444
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C;Accession: S17428
C;Accession: C.J.; Slack, J.L.; Mosley, B.;
R;McMahan, C.J.; Slack, J.K.; Spriggs, M
R;Tominaga, S.; Yokota,
Biochim. Biophys. Acta
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A;Title: A novel IL-1 receptor, cloned from B cells by A;Reference number: S17428; MUID:92007725; PMID:1833184
A;Accession: S17428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interleukin-1 receptor type II - C;Species: Homo sapiens (man) C;Date: 13-Jan-1995 #seconomo row
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S17428
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A; Residues: 1-398 < MCM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --EEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAPPLEVVQKDSC 137
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                                                                                                                                                                                                     RTEDETRTQI ----
                                                                                                                                                                                                                                      ISPLKTI--SASLGSRLTIPCKVFLGTGTPLTTMLWWTAN--
                                                                                                                                                                                                                                                                      HSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINESISHS
                                                                                                                                                                                                                                                                                                       EKFLSVRGTTHLLVHDVALEDAGYYRCVLTFAHEGQQYNITRSIBLRIKKKKEETI-PVI
                                                                                                                                                                                                                                                                                                                                        NVIPEGMNLSPLI---ALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVI 245
                                                                                                                                                                                                                                                                                                                                                                     F----LP----FISYPQILTLSTSGV--LVCPDLSEPTRDKTDVKIQWYKDSLLLDKDN
                                                                                                                                                                                                                                                                                                                                                                                                          FNSPMKLPVHKLYIEY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                       PGEE-----ETRMWAQDGALWLLPALQEDSGTYVCTTRNASYCDXWSIELRVFENTDA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AARSCRFRGRHYKREFRL-EGEPVALRCPQVPYWLWASVSPR----INLTWHKNDSARTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
 , T.; Yanagisawa, K.;
1171, 215-218, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%;
                                                                                                                                                                                                  ----LSIKKVTSEDLKRSYVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 252;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                    GIQRITCPNVDGYFPSSVKPTITWYMGCYKIQNFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cosman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.2e-11
                 Tsukamoto,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                    326
                                                                                                                                                                                                     332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Lupton,
J.E.
                 T.;
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                 Takagi,
                                                                                                                                                                                                                                      DTHIESAYPGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.D.;
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                 Tetsuka,
                                                                                                                                                                                                                                                                      305
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RESULT 12
$42632
Fit-1S protein precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Alternative promoter usage of the A; Reference number: S42632; MUID:94178260; A; Accession: S42632
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A;Molecule type: mRNA
A;Residues: 1-328 <TET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Nucleotide sequence of a complementary DNA for A; Reference number: S30444; MUID:93129624; PMID:1482686
                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergers, G.; Reikerstorfer, A.; Braselmann, MBO J. 13, 1176-1188, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                   olecule type: mRNA esidues: 1-336 <BER>
                          172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312
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                                                                                                                                                                                                                       9
RNTTYCSKVAFPLEVVQK-DSCFNSPMKLPVHKLYIEYG----IQRITCPNVDGYFPSSV 171
                                                                                                                                           QRGGAINPVEWYYSN
                                                                                                                                                                                                                                                        LWCV----VSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYS 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDMVLRIADVKEEDLILQYDCLALNLHGLRRHTVRLSRKNPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPA 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIGKNANLTCSACFGKGTQFLAAVLWQLNGTKITDFGEPRIQQEEGQNQSFSNGLA---C 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVIDNVMTEDAGDYTCKFIHNENGANYSVTATRSFTVKDEQGFSLFPVIGAPAQNEIKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEEPINFR 86
                                                                 RSPESIKTGSLNVTIYKRPPNC-
                                                                                                                                                                              TAHSAGLTLIWYWTRODRDLEEPINFRLP---ENRISKEKDVLWFRPTLLNDTGNYTCML 116
                                                                                                                                                                                                                     LWALAILTVPMYFI-----VTEGRKTSWGL-----ENEALIVRCP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDD----ITIDVTINESISHSRTEDET 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YLMYSTVSGSEKNSKIYCPTIDLY---NWTAPLEWFKNCQALQGSR----YRAHKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HKLYIEYGI-----QRITCPNVDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNLSF 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---NRVFASGQLLKFLFAEVADSGIYTCIVRSPTFNRTGYANVTIYKKQSDCNVFD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVAFPLEVVQKDSCFNSPMKLPV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LI---ALISNNGNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYEK 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 6.3%; Score 229.5; DB 2; Similarity 23.7%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S30444
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                    6.0%; Score 220; DB 2;
23.5%; Pred. No. 6.6e-09;
                                                                                                                                     ----TNERIPTQKRNRIFVSRDRLKFLPAKVEDSGIYTCVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B15R protein;
                                                                                                                                                                                                                                                                                                    62; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56;
                                                             ----KIPDYMMYSTVDGSDKNSKITCPTIALY---NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fos-responsive gene Fit-1 generates mRNA PMID:8131748
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                                                                                                                                                                                                                                                                                                                                    Length 336
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                                                                                                                                                                                                                                                                                               Gaps
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B15R protein precursor - vaccinia virus (strain WR)
C;Species: vaccinia virus
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993
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J. Gen. Virol. 72, 511-518, 1991

A;Title: Two vaccinia virus proteins structurally related to A;Reference number: A38472; MUID:91170931; PMID:1826022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:D01018; NID:g222696; C;Superfamily: vaccinia virus B15R protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: A38472; JQ0929 R;Smith, G.L.; Chan, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;136-196/Domain: immunoglobulin homology <IMM2>
;235-311/Domain: immunoglobulin homology <IMM3>
;48-99;143-194;242-309/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;1-18/Domain: signal sequence #status predicted;19-326/Product: B15R protein #status predicted;41-101/Domain: immunoglobulin homology <IWM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A38472;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: glycoprotein
                                                                                                                                                                       168
                                                                                   224
                                                                                                                                                                                                                  187
                                                                                                                                                                                                                                                           112
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                                                                                                                                                                                                                                                                                                    127 FPLSVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPTITWYMGCYKIQN 186
                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                        67 TLIWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKVA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 VSLYFY-GILOSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGL
                                                                                                                                                                                                                                                                                                                                               DILMEKRGADNDRIIPID-----NGSNMLILNPT-QSDSGIYICITTNETYCDMMS
NKIYMTDKRRVITSRLNINPVKEED-ATTFTCMA 311
                                    HSRTEDETR----TQILSIKKVTSEDLKRSYVCHA
                                                                                   MQLPDGIVT-
                                                                                                                            IHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRN-EVWWTIDGKKPDDITIDVTINESIS 303
                                                                                                                                                                       -NKRLKQRTPGIITIEDVRKNDAGYYTCVLEYIYGGKTYNVTRIVKLEV
                                                                                                                                                                                                                FUNVIPEGMILSFLIALISMN--GNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPV 244
                                                                                                                                                                                                                                                           LNLTIVSVSESNIDLISYP--QIVNERSTGEMVCPNINAFIASNVNADIIW-SGHRRLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                   LSIFFYSSFVQTFNAPECIDKG-QYFASFMELENEPVILPCPQI-NTLSSGYNI----L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARSAKGEVAKAAKVKOKVPAPRYTVELA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKKPDDITIDVTINESISHSRTEDE-----TRTQILSIKKVTSEDLKRSYVCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAPVQWFKNCKALQG-----PRFRAHMSYLFIDKVSHVDEGDYTCRFTHTENGTNYIVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRSFTVEEKGF---STPPVITNPPHNYTVEVEIGKTANIACSACFGTASQFVAVLW----
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                                                                                 --SIGSNLTIACRV--SLRPPTTDADVFWISNGMYYEEDDGDGNGRISVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 189; DB 1;
Pred. No. 1.4e-06;
0; Mismatches 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunoglobulin
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interleukin-1 beta : C;Species: vaccinia

receptor

vaccinia virus

(strain

Ankara)

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3ULT
T20992
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                                                                                                                                                          submitted to the EMBL Data Library, A;Reference number: Z19929
A;Accession: T24733
                                                                                                                                                                                                                                      A; Molecula v.f.
A; Residues: 1-5175 (MIL)
A; Cross-references: EMBL: Z47068; P
A; Cross-references: clone F1569
                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A;Reference number: Z19355
A;Accession: T20992
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                                                                                               A; Molecule type: DNA
A; Residues: 1-5175 <WI2>
                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                            R;Sulston,
                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F15G9.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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A;Experimental source: strain Ankara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-326 < ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Variety: strain Ankara
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: T37450
                                                           Experimental source: clone T09B9
                                                                          Cross-references: EMBL: Z47070; PIDN: CAÁ87344.1; GSPDB: GN00028; CESP:F15G9.4a
                                                                                                                                                                                                                                                                                                                                                                                                                               Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: T37450
                     Gene: CESP:F15G9.4a
                                        Genetics:
                                                                                                                                         Status: preliminary; translated from GB/EMBL/DDBJ
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position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DILWEKRGADNDRIIPID------NGSNMLILNPT-QSDSGIYICITNETYCDMMS
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                                                                                                                                                                                                                                                                PIDN:CAA87335.1; GSPDB:GN00028;
                                                                                                                                                                                                     December 1994
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Best Local Similarity
Matches 141; Conserv
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                                                                                                                                                                                     -----VFTPPVVSVKSDNPIKALGETITLFCNAS------GNPYP---QLK
                                                                                                                                                                                                                          RSRRMIVVLSPDYVTEKS---ISMLEFKLGVMCQNSIATKLIVVBYRPLEHPHPGILQLK 516
                                                                                                                                                                                                                                                                                                                                     NDVQPQVAVNQPTIMRCA-----VTGHPFPSIKWLK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPTI------KREGDTITLTCPIKLAEDIADQVMDVSWTKDSRALDG---DLTDN
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 RAEIHNOPOWETHLCKPVPOESETOWIONGTRLEPPAPOISALALHHFTDLSN
                                                                          DHVQRRSRLKEPPELQSSERAAGSPPAPGXMSKHRGKSSATCRCCVTYCEGENHLRNKS
                                                                                                              WAKGGSLIFDSPDGARISLKGA
                                                                                                                                               ----ESVSFVSWKGEKSKHSGSKFWKALRLALP-LRSLSAS----SGWNESCSSQSDISL 567
                                                                                                                                                                                                                                                            GKE----VIDDENIRIVEQGQVLQILR-TDSDHAGKWSCVAENDA--GVKELEMVLD---
                                                                                                                                                                                                                                                                                                GKEYDIYVSYARNAE--EEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQ 459
                                                                                                                                                                                                                                                                                                                                                                                                           VDIS-----DDGRKLTISQASLENAGL---YTCIALNRAGEASLEFKVEILSPPVIDISR
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                                      -----VLVPPEI-NRDGIDMSPRLP-----AQQSLTLQC---LAQG-----
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21.6%; Pred. No. 7.3e-05;
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                                                                                                              RLDIPHLKKTDVGDYTCQALNAAGTŠEASVŠV
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Search completed: April 23, 2003, 08:54:58 Job time : 56 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2003 Compugen Ltd.
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bos taurus
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P13504;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-1 receptor, type I precursor (IL-ILIR1 OR ILIRA OR IL-1R1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDTGNYTCMLRNTTYCSKVAFPLEVVQKDS--CFNSPMKLPVHKLYIEYGIQRITCPNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYQGKQYPVTRVITFITIDDSKRD-RPVIMSPRNETM-EADPGSTIQLICNVTGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENGRIFHLIRTLIVKVVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - FFKDENNELPKVQWYKNCKPLP-----LDDGNFFGFKNKLMVMNVAEEHRGNYTCRTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDSGYYYCIMRNSTYCLKTKITMSVLENDPGLCYNTQASF-IQRLHVA-GDGSLVCPYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CPLTPNEMH------GTIIWY----KNDSKTPISAD-KDSRIHQQNEHLWFVPAKM
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                                                                                                                                                                                                    QRRS-----
                                                                                                                                                                                                                                 RSLSASSGWNESCSSQSDISLDHVQRRRSRLKEPPEL
                                                                                                                                                                                                                                                                       IILLELEKIQDYE----KMPESIQFIKQKHGAICWSGDFKERPQSAKTRFWKNLKYQMPA
                                                                                                                                                                                                                                                                                                           LIVVEYRPLEHPHPGILQLKESVSFVS-----WKG---EKSKHSGSKFWKALRLALPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNT--HILETAHVRLVYPVPDFKNYLIGGFAIFTATAVFCACIYKVFKVDIVLWYRDSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TDLVYWKWNGSEIEWDDPILAEDYQFLEHPSAKRKYTLITTLNVSEVKSQFYRYPFICFV
                                                                                                                                                                                                                                                                                                                                                 GEDTIEVTNENVKRSRRLIIILVRD-----MGSFSCLGQSSEEQIAIYDALIREGIK
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IG-LIKE C2-TYPE I
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   PHOSPHORYLATION OF THR-556.

MEDINE=91254338; PubMed=1828344;

A Bird T.A., Woodward A., Jackson J.L., Dower S.K., Sims J.B.;

A Bird T.A., Woodward A., Jackson J.L., Dower S.K., Sims J.B.;

I merieukin 1 receptor at a single threonine residue.";

E Biochem. Biophys. Res. Commun. 177:61-67(1991).

C -!- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (II.

C -!- FUNCTION: TRECEPTOR ANTAGONIST PROTEIN (IL-1RA). BING

C AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA). BING

C -!- SUBCELLULAR ICCATION: Type I membrane protein.

C -!- SUBCIELLURAR ICCATION: Type I membrane protein.

C -!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR004076; IL1R_receptor.
InterPro; IPR004076; IL1 receptor1.
InterPro; IPR004074; IL1 receptor1/II.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_like.
InterPro; IPR00300; Ig_like.
InterPro; IPR000157; TIR_domain.
Pfam; PF001592; TIR; 1.
                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01538; INTRLEUKN1R1.
PRINTS; PR01536; INTRLKN1R12F.
PRINTS; PR01537; INTRLKN1R1F.
SMART; SM00410; IG like; 1.
SMART; SM00255; TIR; 1.
PROSITE; PS50104; TIR; 1.
Immunoglobulin domain; Receptor; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 20-73.

MEDLINB=88290679; PubMed=2969618;
Sims J.E., March C.J., Cosman D., Widmer M.B., McDonald H.R.

Sims J.E., March C.J., Cosman D., Widmer M.B., McDonald H.R.

McMahan C.J., Grubin C.E., Wignall J.M., Jackson J.L., Call

Friend D., Alpert A.R., Gillis S., Urdal D.L., Dower S.K.;

Friend D., Alpert A.R., Gillis S., Urdal D.L., Dower S.K.;
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Bukaryota; |
Mammalia; E
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[2]
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PIR; A32604; A32604.
HSSP; P14778; 1IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "cDNA expression cloning of the IL-1 immunoglobulin superfamily."; Science 241:585-589(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P14778; 1IRA.
MGD; MGI:96545; Illr1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a conveen the Swiss Institute of Bioinformatics and the EMBL of Burppean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and foittes requires a license agreement (See http://www.isb-sib.esend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                              Phosphorylation.
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Eutheria;
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Rodentia;
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IR SIMILARITY.
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Best Local
receptor.";
Nucleic Aci
[2]
                                                                                                                                            15-JUN-2002 (Rel. 14, Last sequence update)
Interleukin-1 receptor, type I precursor (IL-IR-1) (IL-IR-alpha)
(P80) (Antigen CD121a).
ILIRI OR ILIRA OR ILIR.
Homo sapiens (Humana)
                                                                                                                                                                                                                      IL1R HUMAN
P14778;
01-APR-1990
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CARBOHYD
MOD_RES
                                    MEDLINE=90098789; PubMed=25323231
Chua A.O., Gubler U.;
"Sequence of the cDNA for the hu
                                                                                                                                  Homo sapiens (Human
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                            HUMAN
                                                                                     SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=9606;
                                                                                                                       Mammalia; Eutheria;
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               Acids Res. 17:10114-10114(1989).
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25.8%;
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Pred. No. 3.7
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N-LINKED (GLCNAC. . .)
PHOSPHORYLATION (BY PKC)
                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                    fibroblast
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                                    type interleukin-1
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PIR; S06928; S06928.
PIR; A36187; A36187.
PDB; 11TB; 04-FEB-98.
PDB; 11RA; 17-JUN-98.
DOMAIN
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DISULFID
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PRINTS; PR01536; INTRLKNIR12F;
PRINTS; PR01537; INTRLKNIR1F.
SMART; SM00410; IG like; 1.
SMART; SM00255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90046906; PubMed=2530587;
Sims J.E., Acres R.B., Grubin C.E., McMahan C.J.
March C.J., Dower S.K.;
"Cloning the interleukin 1 receptor from human T
Proc. Natl. Acad. Sci. U.S.A. 86:8946-8950(1989)
                                                                                                                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A., Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.; "A new cytokine-receptor binding mode revealed by the crystal structure of the IL-1 receptor with an antagonist.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS)
MEDLINE=97215904; PubMed=9062194;
Schreuder H., Tardif C., Trump-Kallmey
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X16896; CAA34773.1;
EMBL; M27492; AAA59137.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                      PROSITE; PS50104; TIR;
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                                                                                                                                                                                                                                                                                                   InterPro;
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MIM; 147810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vigers G.P., Anderson L.J., Caffes P., Brandhuber B.J.;
"Crystal structure of the type-I interleukin-1 receptor complexed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
MEDLINE=97215903; PubMed=9062193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=T-cell;
                                                                                                                                                      Immunoglobulin domain;
                                                                                                                                                                                                                                                                                                                                                           fnterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA AND INTERLEUKIN-I RECEPTOR ANTAGONIST PROTEIN (IL-1RA). THE AGONIST LEADS TO THE ACTIVATION FOR PKAPPA B. SUBCELLULAR LOCATION: Type I membrone protein. SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAI SIMILARITY: CONTAINS 1 TIR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DATABASE: NAME-PROW; NOTE=CD guide CD121a entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd121a.htm".
                                                                                                                                                                                                                                                                                                                                                                                      HGNC:5993; IL1R1.
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                                                                                                                                          3D-structure.
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; IPR004075; I
; IPR004074;
; IPR003006;
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17
569
336
356
569
103
203
319
541
                                                                                                                                                                                                                                                                                ; ILIR_receptor.
; ILI_receptor1.
; ILI_receptor1/II.
; IG_MHC.
; Ig_like.
; TIR_domain.
                                                                                                                                                       Transmembrane; Glycoprotein; Receptor;
           INTERLEUKIN-1 RECEPTOR, EXTRACELLUAR (POTENTIAL).
POTENTIAL,
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1
IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 3
TIR.
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                                                                                                (POTENTIAL)
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                                                                                                               TYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BETA (IL-1B),
VA). BINDING TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WITH IL1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                       Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 129
                                                                                                                                          TL1S MOUSE
P27931;
01-AUG-1992
01-AUG-1992
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
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                                                                                                        01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-1 receptor, type II precursor (IL-IR-2)
ILLR2 OR ILLRB OR IL-IR2.
Mus musculus (Mouse).
  SEQUENCE FROM N.A.

MEDLINE=92007725; PubMed=1833184;

McMAhan C.J., Slack J.L., Mosley B., Cosman D., Lupton S.D.,

McMahan C.J., Grubin C.B., Wignall J.M., Jenkins N.A., Brannan

Copeland N.G., Huebner K., Croce C.M., Cannizzarro L.A., Benjan

Dower S.K., Spriggs M.K., Sims J.E.;
                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                   MOUSE
                                                                                                                                                                                                                                                                514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKPTRPVIVSPANE--TMEVDLGSQIQLICNVTGQL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGCYKIQNFNNVIPEGMNLSFLIALIS--NNGNYTCVVTYPENGRTFHLTRTLTVKVVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPLEVVQKDS--CFNS----PMKLPVHKLYIEYGIQRITCPNVDGYF--PSSVKPTITWY
                                                                                                                                                                                                                                                                                                                                                                        VTNPQKHM---IGICVTLTVIIVCSVPIYKIFKIDIVLWYRDSCYDFLPIKASDGKTYDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITWY----KDDSKTPVSTB-QASRIHQHKEKLWFVPAKVEDSGHYYCVVRNSSYCLRIK 108
                                                                                                                                                                                                                                         QLKESVSFVS-----WKGEKS---KHSGSKFWKALRLALPLRSLSASS
                                                                                                                                                                                                                                                                                     RRLIIILVRETSGFSWLGGSSEEQIAM----XNALVQDGI--KVVLLELEKIQDYB----
                                                                                                                                                                                                                                                                                                                                                                                     KDC-KPLLLDNIHFSGVKDRLIVMVVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   I SAKEVENE PNLCYNAQA I FKOKLPV-----AGDGGLVCPYME-FFKNENNELPKLQWY
                                                                                                                                                                                                                                                                                                         RRMIVVLSPDY---
                                                                                                                                                                                                                                                                                                                                YILYPKTVGEGSTSDCDIFVFKVLPEVLEKQCGYKLFIYGRDDYVGEDIVEVINENVKKS
                                                                                                                                                                                                                                                                                                                                         YVSYARNAEE-----EEFVLLTLRGVLENEFGYKLCIFDRDSLFGGNTVEAVFDFIQRS
                                                                                                                                                                                                                                                                                                                                                                                                                    VLGEDYYSVENPANKRRSTLITVLNISEIESRFYKHPFTCFAKNTHG--IDAAYIQLIYP
                                                                                                                                                                                                                                                                                                                                                                                                                                           TINESI ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSPLMDSRNEVWWTIDGKKPDDITIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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121
142
248
100
193
233
233
249
263
297
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVP
                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
164
196
312
312
100
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193
233
233
249
263
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                                                                                      Chordata;
Rodentia;
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N-LINKED
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Pred. No. 1.
                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5BAA83F8F0225C25
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                                                                                                                                                                                        410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDIAYWKWNGSVIDE--DDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                 553
                                                                                                                                                                                                                                            547
               Benjamin
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             C.I.,
min D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                          387
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Query Match
Best Local S
Matches 102
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DISULFID
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TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR01539; IN PRINTS; PR01536; IN SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A novel II-1 receptor, cloned from B cells by mammalian is expressed in many cell types.";
EMBO J. 10:2821-2832(1991).

-i- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A),
-AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1A)
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X59769; CAA42440.1; -. MGD; MGI:96546; Illr2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR004074;
InterPro; IPR004077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003599; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599;
311
                               307
                                                                 253
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hes 102;
                                                                                                                                                                                                                                                                              92
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                                                                                                                                                                                                                                                                                                                                                                                22
SENDENYVEVSLIFDPVTREDLHTDPKCVASNPRSSQSLHTTVKEVSSTPSWSIALA---
                                                                 SPLETI--PASIGSRLIVPCKVFLGTGTSSNTIVWWLANSTFISAAYPRGRVTEGLHHQY
                                                                                                                                 SFLIA-----LISNN-----GNYTCVVTYPENGRTFHLTRTLTVKVVGSPKNAVPPVIH
                                                                                                                                                                                                        ASLP-HVSYLQISALSTTGLLVCPDLKEFISSNADGKIQWYKGA-----ILLDKGNK
                                                                                                                                                                                                                                         MKLPVHKLYIEYGIQRIT---
                                                                                                                                                                                                                                                                                                PINFRLPENRISKEKDVLWFRPTILADTGNYTCMLRNTTYCSKVAFPLEVVQKDSCFNSP 141
                                                                                                                                                                                                                                                                                                                                               DNCQFRGREFKSELRL-EGEPVVLRCPLAPH---SDISSSHSPLT----WSKLDSSQLI
                                                                                                                                                                                                                                                                                                                                                                                  ERCDDWGLDTWRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEE
                               TE-DETRTQI-LSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQKVPAPRYTVELACGP
                                                                                                SPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINESISHSR
                                                                                                                                                                                                                                                                               PRD----EPRMWVKGNILWILPAVQQDSGTYICTFRNASHCEQMSVELKVFK----
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR01539; INTRLEUKN1R2
PR01536; INTRLKN1R12F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
14
356
382
382
157
157
263
270
124
208
231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain; Receptor; Glycoprotein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13
410
355
381
410
127
226
345
120
120
219
338
124
208
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                                                                                                                                                                                                                                                                                                                                                                                                                                   8.6%;
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IL1_receptorIIp.
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                                                                                                                                                                                                                                                                                                                                                                                                                     73;
                                                                                                                                                                                                                                             -CPNVDGYFPSSVKPTITWYMGCYKIQNFNNVIPEGMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERLEUKIN-1 RECEPTOR,
EXTRACELLULAR (POTENTIAL)
POTENTIAL
POTENTIAL
CYTOPLASMIC (POTENTIAL)
LIG-LIKE C2-TYPE DOMAIN 1
LIG-LIKE C2-TYPE DOMAIN 2
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C2-TYPE DOMAIN 3
LIG-LIKE C4-CYPE
LIG-LIKED (GLCNAC. . . )
N-LINKED (GLCNAC. . . )
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 314; DB 1; Pred. No. 2.1e-16; 3; Mismatches 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          923DFC27C70AF604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                      164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L-1A), BETA (IL-1RA).
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL)
(POTENTIAL)
(POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE
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                                                                                                                                                                                                                                                                               -NTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                     91
                                                                     310
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365

GATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDI 407

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RESULT 5
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            Query Match
Best Local :
  Matches
                                               CARBOHYD
CARBOHYD
SEQUENCE
                                                                                              DISULFID CARBOHYD
                                                                                                                      DISULFID
                                                                                                                                                                                                                                                            Repeat.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Interleukin-1 stimulates the expression of type I and t interleukin-1 receptors in the rat insulinoma cell line sequencing a rat type II interleukin-1 receptor cDNA."; Eur. Cytokine Netw. 5:319-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interleukin-1 receptor, type II precursor (IL-1R-2).
ILIR2 OR ILIRB OR IL-1R2.
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rati
                                                                                     CARBOHYD
                                                                                                                                                            DOMAIN
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                  InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z22812; CAA80465.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=95035882; PubMed=7524717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P43303;
01-NOV-1995
                                                                                                                                               DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004074; IL1_receptorI/II.
InterPro; IPR004077; IL1_receptorIIp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bartfai T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10116;
                                                                                                                                                                                                                                                         Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL1S RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 ---PLSLIILVV--GAIWMRRRCKRRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J., Gatti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 32, Created)
(Rel. 32, Last sequence up
(Rel. 41, Last annotation
  Conservative
                                               A,
                                                                                                                                                                                                                                                        domain;
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            8.2%;
                                                 46353
                                                                                                                                                                                                                                                       Receptor; Glycoprotein; Transmembrane;
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                                                 MW.
                                          POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1

IG-LIKE C2-TYPE DOMAIN 3

IG-LIKE C2-TYPE DOMAIN 3

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

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N-LINKED (GLCNAC...) (()
 67;
Score 302; DB 1;
Pred. No. 1.7e-15;
7; Mismatches 15;
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                   POTENTIAL.
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 153;
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                     Length 416;
                                               CRC64;
Indels
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Yd
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                                                                                   EMBL; U64092;
EMBL; U64093;
HSSP; P14778;
                                                                                                                                                                                                                                                                                            -i- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A), BETA (IL-1B), AND INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
-i- SUBCELLULAR LOCATION: THE LONG ISOFORM IS A TYPE I MEMBRANE PROTEIN WHILE THE SHORT ISOFORM IS SOLUBLE.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96355446; PubMed=8702856;
Liu C., Hart R.P., Liu X.J., Clevenger W., Maki R.A., Souza "Cloning and characterization of an alternatively processed type II interleukin-1 receptor mRNA.";
J. Biol. Chem. 271:20965-20972(1996).
                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q29612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.,
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15-JUN-2002
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                                                                        nterPro;
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IPR004074; IL1_receptorI/II.
IPR004077; IL1_receptorIIp.
IPR003599; Ig.
IPR003006; Ig_MHC.
IPR003600; Ig_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPRMWVKDDTLWVLPAVQQDSGTYICTFRNASHCEQMSLELKVFK-----NTEA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
1 receptor, type II precursor (IL-1R-2)
                                                                                                       AAB05876.1; -.
AAB05877.1; -.
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                                                                                                                                                                                                          as its content
                                                                                                                                                                        . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IL-1R-beta).
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                                         .-AUG-1992 (Rel. 23, Created)
15-JUN-2002 (Rel. 24, Last sequence upd.
Interleukin-1 receptor, type II precurso
(Antigen CDw121b).
IIIR2 OR ILIRB.
Homo sapiene 'The Street of the Stree
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Best Local S
Matches 89
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
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PRINTS; PR01536; INTRLKN1R12F.
SMART; SM00409; IG; 2.
SMART; SM00410; IG like; 1.
Immunoglobulin domain; Receptor;
                                                                                                                                                                                                                                       MAMUH.
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                  ; Chordata;
; Primates;
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IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

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Pred. No. 2.1e
64; Mismatches
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EXTRACELLULAR
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                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                              ence update)
tation update)
precursor (IL-1R-2)
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.1e-12;
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(POTENTIAL).
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                                                                                                                    (IL-1R-beta)
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Chou H.-H., Takashiba T., Takigawa M., Maeda H., Asamura
Chou H.-H., Arai H., Murayama Y.;

"Complete nucleotide sequence and expression of the human
"Complete nucleotide sequence and expression of the human
interleukin-1 receptor type II in human gingival fibrobli
interleukin-1 (ncm-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mead K., Maupin R., Yoakum M., Hotic M.;
"The sequence of Homo sapiens BAC Colone RP11-451C2.";
"The sequence of Homo sapiens BAC colone RP11-451C2.";
Submitted (MAR-1999) to the EMBL/GenBank/JDBJ databases.
--!- FUNCTION: RECEPTOR FOR INTERLEUKIN-1 ALPHA (IL-1A),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McMahan C.J., Slack J.L., Mosley B., Cosman D., Brunton L.L., Grubin C.E., Wignall J.M., Jenkin Copeland N.G., Huebner K., Croce C.M., Cannizza Dower S.K., Spriggs M.K., Sims J.E., "A novel IL-1 receptor, cloned from B cells by is expressed in many cell types.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a celebrate the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
TISSUE=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND INTERLEUXIN-1 RECEPTOR ANTAGONIST PROTEIN (IL-1RA).
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DATABASE: NAME=PROW; NOTE=CD guide CDw121b entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cdw121b.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Cosman D., Lup
J.M., Jenkins N.,
M., Cannizzarro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammalian expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lupton S. IS N.A., Br
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Brannan
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EMBL; X59770; CAA42441.1; --. EMBL; U74649; AAD00242.1; --. EMBL; AC007165; AAK52072.1; PIR; S17428; S17428. HSSP; P14778; 11TB. MIM; 147811; Genew; InterPro; InterPro; interPro; IPR004074; IL1\_receptorI/II. interPro; IPR004077; IL1\_receptorIIp. HGNC:5994; IL1R2. IPR004077; IPR003599; IPR003599; Ig. IPR003006; Ig\_MHC.

Immunoglobulin Repeat. SIGNAL 1

PRINTS; PRO1539; INTRLEUKN1R2 PRINTS; PRO1536; INTRLKN1R12F SMART; SM00409; IG; 3.

domain;

Receptor;

Glycoprotein;

Transmembrane;

Signal;

Pfam;

PF00047; ig;

nterPro;

CHAIN DOMAIN

INTERLEUKIN-1 EXTRACELLULAR

(POTENTIAL)

TYPE

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CONFLICT

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1

IG-LIKE C2-TYPE DOMAIN 2

IG-LIKE C2-TYPE DOMAIN 3

145 251 50 152 258 258 66 72 72 112 219 277 123

IG-LIKE C2-TYPE
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Best Local S
Matches 79
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15-JUN-2002
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SEQUENCE
      Klemenz R., Hoffmann S., Werenskiold A.K.; of a gene with s. "Serum- and oncoprotein-mediated induction of a gene with s. similarity to the gene encoding carcinoembryonic antigen."; Proc. Natl. Acad. Sci. U.S.A. 86:5708-5712(1989).
-!- FUNCTION: POSSIBLY INVOLVED IN REGULATION OF T-LYMPHOCY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BSDOM
                                                                                                           "Molecular cloning of the murine chromosomal mapping.";
Biochim. Biophys. Acta 1090:1-8()
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                     STRAIN=C3H/He; TISSUE=Spleen;
MEDLINE=91355215; PubMed=1832015;
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 "A putative protein is highly similar to receptor.";
                                                                                                                                                                                                                                                                                    MEDLINE=90092495;
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                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin 1 receptor like 1 precursor (ST2)
                                                                      MEDLINE=89345536; PubMed=2527364;
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                retsuka T.;
                                                                                                                                                                                                                                                                         Cominaga S.;
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398 i
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Rodentia;
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                                                                                                            1090:1-8(1991)
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            T-LYMPHOCYTE
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SMART; SM00408; IGC2; 1.
Immunoglobulin domain; Glyco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S30444; S30444.
Genew; HGNC:5998; IL1RL1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Nucleotide sequence of a complementary DNA for human ST2."; Biochim. Biophys. Acta 1171:215-218(1992).
-!- FUNCTION: POSSIBLY INVOLVED IN REGULATION OF T-LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003598;
InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM; 601203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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-!- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tersuka
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Tominaga S.-I., Yokota T., Yanagi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Lymphocytes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interleukin 1
IL1RL1 OR ST2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domo sapiens (Human)
27 WGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAGLTLIWYWTRQDRDLEEPINFR 86
                                                            81;
                                                                              Similarity
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1 receptor-like 1 precursor (ST2
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(Rel. 25, Last sequence up)
(Rel. 41, Last annotation
                                                            Conservative
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Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yanagisawa K., Tsukamoto
                                                                                                                                                                                                                                                                                                                  INTERLEUKIN 1 RECEPTOR-LIKE 1
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
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Pred. No. 4e-10;
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                                                                                                                                        F91C47EA2D7FE811 CRC64;
                                                              Mismatches
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(GLCNAC...
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                                                            Indels
                                                                                               Length 328;
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                                                            Gaps
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PIR; A38472; WMVZ15. PIR; JQ1809; JQ1809.

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VACCV
                                                                                                                                                                                                                                                                             interleukin-1 receptor and the immunoglobulin superfamily.";
J. Gen. Virol. 72:511-518(1991).
-!- FUNCTION: BINDS INTERLEUKIN-1 AND POSSIBLY INTERLEUKIN-6.
-!- PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS.
CONSEQUENCE THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91259063; PubMed=2045793; Smith G.L., Chan Y.S., Howard S.T.; "Nucleotide sequence of 42 kbp of vaccinia virus the right inverted terminal repeat."; J. Gen. Virol. 72:1349-1376(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VB16_VACCV
P25212;
                                      EMBL; D11079; BAA01845.1; -. EMBL; A19577; CAA01477.1; -. EMBL; D01018; BAA00825.1; -.
                                                                                           entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B16R OR B15R.
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15-JUN-2002
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                    Smith G.L., Chan Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orthopoxvirus
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                                                                                                                                                   the European Bioinformatics Institute.
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                                                                                                                                                                                                                                      VIRUS REPLICATION ENHANCED SUBCELLULAR LOCATION: VIRIC GLYCOPROTEIN.
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Last annotation update)
protein precursor (Prot
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VB16 COWPX
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15-JUN-2002
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SEQUENCE FROM N.A.
STRAIN-Brighton red;
MEDLINE=93008237; PubMed=1339315;
Spriggs M.K., Hruby D.E., Malisze
Sims J.E., Buller R.M.L., Vanslyk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
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PRINTS; PR01540; INTRLKUKN1BP.
PRINTS; PR01536; INTRLKN1R12F.
SMART; SM00409; IG; 2.
SMART; SM00410; IG_like; 1.
                                                                                  B16R OR B15R.
Cowpox virus (CPV).
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SIGNAL 1
                                                                Orthopoxvirus.
                                                                         Viruses; dsDNA viruses,
                                                      NCBI_TaxID=10243;
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IPR003006;
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Pred. No. 4.8e-07;
0; Mismatches 156;
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SIGNAL 1
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PRINTS; PR01540; INTRLEUKN1BP.
PRINTS; PR01536; INTRLKN1R12F
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InterPro; IPR004074; IL1_receptorI/II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding protein.";
Cell 71:145-152(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003599;
InterPro; IPR003006;
InterPro; IPR003600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch)
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279
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                                                                                                                                                                                                                                                                                           FUNCTION: BINDS INTERLEUKIN-1 AND POSSIBLY INTERLEUKIN-6. PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS. CONSEQUENCE THE INFLAMMATORY RESPONSE WOULD BE DIMINISHED
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SIMILARITY: C
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                                                                                                          NKI YTTDKRRVITSRLKINPVKEED-ATTFTCMA
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                       SHSRTEDETR---TQILSIKKVTSEDLKRSYVCHA
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SM00410; IG_like;
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IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
IG-LIKE C2-TYPE DOMAIN
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N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
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Pred. No. 6.8e-
50; Mismatches
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N-LINKED (GLCNAC...
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311
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or send a
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SEQUENCE FROM N.A.
MEDLINE=91021027; PubMed=2219722;
MEDLINE=91021027; Johnson G.P., Perkus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
15-JUN-2002
                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EWBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Appendix to 'The complete Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete DNA sequence Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goebel S.J., Johnson Paoletti E.;
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InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2 SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTOR CAUTION: This is a conceptual translation; a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: BINDS INTERLEUKIN-1 AND POSSIBLY INTERLEUKIN-6. COULD PREVENT THESE CYTOKINES REACHING THEIR NATURAL RECEPTORS. IN
                                                                                                                                                                                                                                                                                                                                                                            readover in position 31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            VIRUS REPLICATION ENHANCED.
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SM00410; IG_like;
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA stage; Poxviridae;
                                                                                                      INTERLEUKIN-1 BINDING PR
IG-LIKE C2-TYPE DOMAIN 1
IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 3
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED
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(GLCNAC...)
(GLCNAC...)
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TLR1_MOUSE
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Q9EPQ1; Q9EPW5;
15-JUN-2002 (Rel
                                                 STRAIN-BALB/c; TISSUE-Spleen;
Thomson D.P., Campbell C.C., Liew F.Y., Xu D.,
"Cloning of Mus musculus Toll-like receptor 1.";
"Cloning of Mus musculus Toll-like receptor 1.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Participates in the innate immune response to agents. Cooperates with TLR2 and modulates the response microbial constituents. Acts via MyD88 and TRAF6, leading microbial constituents.
                                                                                                                                                                                                                                                                                                                             Ozinsky A., Underhill D.M., Fontenot J.D. Wilson C.B., Schroeder L., Aderem A.; "The repertoire for pattern recognition immune system is defined by cooperation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Toll-like receptor 1 precursor (Toll/interleukin-1
                                                                                                                                                                                                       Hajjar A.M., O'Mahony D.S., Ozinsky A.,
Klebanoff S.J., Wilson C.B.;
"Functional interactions between Toll-1:
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Mammalia; Eutheria;
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                                                                                                                                                    SEQUENCE FROM N.
                                                                                                                                                                                                                                                TISSUE=Macrophage;
MBDLINE=20571875; PubMed=11123271;
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    receptors.";
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response (By similarity).
SUBUNIT: Binds TLR2 via their
Binds MyD88 via their respecti
                                        kappa-B activation, cytokine secretion
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Sciurognathi;
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IPR000483; LRR_Cterm
IPR003592; LRR_out.
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rane; Repeat; Leucine-rich repeat; Glycoprotein.
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EXTRACELLULAR (POTENTIAL)
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                     WEDLINE=90*40...
Yang R.-B., Mark M.R., Gray A., Huang A., A.c.
Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
Goddard A., Wood W.I., Gurney A.L., Godowski P.J.;
Goddard A., warentor-2 mediates lipopolysaccharide-induced
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=98118556; PubMed=9435236;
Rock F.L., Hardiman G., Timans J.C.,
"A family of human receptors structu
Toll.";
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Dast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98261424; PubMed=9596645;
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                                                                                                                                                                     SEQUENCE FROM N.A.,
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structurally related
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Catarrhini; Hominidae;
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Homo.
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Pfam; PF01463; LRRCT; 1.
Pfam; PF01582; TIR; 1.
SMART; SM00082; LRRCT; 1.
SMART; SM00369; LRR TYP; 2.
SMART; SM00255; TIR; 1.
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RESPONSE TO
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Aliprantis A.O., Yang R.-B., Mark M.R., Suggett S., Devaux B., Radolf J.D., Klimpel G.R., Godowski P.J., Zychlinsky A.;
"Cell activation and apoptosis by bacterial lipoproteins throu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
InterPro;
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SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

TISSUE SPECIFICITY: Highly expressed in peripheral blood leukocytes, in particular in monocytes, in bone marrow, lymph now and in spleen. Also detected in lung and in fetal liver. Levels are low in other tissues.

PTM: N-glycosylated (By similarity).

SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.

SIMILARITY: CONTAINS 14 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ure 408:111-115(2000).

FUNCTION: Cooperates with MD-2 to mediate the innate immune FUNCTION: Cooperates with MD-2 to mediate the innate immune response to bacterial lipoproteins and other microbial cell wall components. Acts via MyD88 and TRAF6, leading to NF-kappa-B activation, cytokine secretion and the inflammatory response. May also promote apoptosis in response to lipoproteins. Recognizes mycoplasmal macrophage-activating lipopeptide-2kD (MALP-2), soluble tuberculosis factor (STP), phenol-soluble modulin (PSM) and B.burgdorferi outer surface protein A lipoprotein (OspA-L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cooperatively with
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ine-rich repeat; Glycoprotein;
POTENTIAL.
TOLL-LIKE RECEPTOR 2.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
LRR 1.
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BAPPARU

TILR6 HUMAN STANDARD; PRT; 796 AA. 09Y2C9; (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Toll-like receptor 6 precursor.

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                                EWCKYELDFSHFRL--FDENNDAAILILLEPIEKKAIPORFCKLRKIMNTKTYLEWPMDE
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HSSP; O60603; 1FYW.
Genew; HGNC:16711; TLR6.
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MEDLINE=99250250; PubMed=10231569;
MEDLINE=99250250; PubMed=10231569;
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Jenkins N.A., Takeda K.,
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Mammalia; Eutheria;
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SUBUNIT: Binds TLR2 via their respective extracellular domains.
Binds MyD88 via their respective TR domains (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein. Plasma membrane phagosomes (By similarity).
TISSUE SPECIFICITY: Detected in monocytes, CD11c+ immature dendritic cells, plasmacytoid pre-dendritic cells and dermal microvessel endothelial cells.
SIMILARITY: BELONGS TO THE TOLL-LIKE RECEPTOR FAMILY.
SIMILARITY: CONTAINS 13 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Participates in the innate immune response to Gram-
positive bacteria and fungi. Acts via MyD88 and TRAF6, leading
NF-kappa-B activation, cytokine secretion and the inflammatory
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; IPR001611; LRK.
; IPR001483; LRR_Cterm.
;: IPR003592; LRR_out.
o; IPR000157; TIR_domain.
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cine-rich repeat; Glycoprotein.
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TOLL-LIKE RECEPTOR 6.
EXTRACELLULAR (POTENTIAL).
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                  PHPGILQLKESVSFVSWKGEKSKHSGSKFWKALRLALPLR 547
                                                                            FHAFISYSEH--DSAWVKSELVPYLEKE-DIQICLHERNFVPGKSIVENIINCIEKSYKS
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Search completed: April 23, 2003, 08:52:18 Job time : 32 secs

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Q9vjx9	Q9VJX9	v	795	5.2	192.5	40
Q9xzf9	Q9XZF9	ഗ	795	5.2	192.5	39
Q9nbk8	Q9NBK8	տ	795	5.2	192.5	38
Q8wre2	Q8WRE2	υ	1356	5.4	196.5	37
Q9j1z8	Q9JLZ8	11	409	5.8	214	36
	Q62612	11	336	6.0	220	35
. Q9h733	Q9H733	4.	410	6.1	222.5	34
	Q9DEE3	13	321	6.2	228	ω ω
Q9dee6	Q9DEE6	13	321	6.2	228	32
O	Q9N2H5	σ	403	6.5	239.5	31
	Q62692	11	280	7.0	258	30
	Q8QFN4	13	571	9.5	347.5	29
	Q9DEE2	13	486	10.6	390	28
Q9dee4	Q9DEE4	13	486	10.6	390	27
Q9er66	Q9ER66	11	354	11.7	428.5	26
Q13525	Q13525	4	562	12.1	444.5	25
Q9hb29	<b>Q9</b> НВ29	4	575	12.1	445.5	24
Q9z2b1	Q9Z2B1	11	614	12.2	446	23
Q62929	Q62929	11	561	12.5	457	22
Q9dee1	Q9DEE1	13	533	12.5	457.5	21
	Q9DEE5	13	533	12.5	457.5	20
Q9uq44	Q9UQ44	4.	556	12.6	463.5	19
Q9ers7	Q9ERS7	11	574	12.7	466	18
Q62611	Q62611	11	566	12.8	470	17

## ALIGNMENTS

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RESULT 1
SEQUENCE FROM N.A.

MEDLINE=20361666; PubMed=10799889;
Jensen L.E., Muzio M., Mantovani A., Whitehead A.S.;

"IL-1 signaling cascade in liver cells and the involvement soluble form of the IL-1 receptor accessory protein.";

J. Immunol. 164:5277-5286(2000).
                                                                                          SEQUENCE OF 118-179 FROM N.A.

MEDLINE=98140136; PubMed=9479509;

Dale M., Hammond D.W., Cox A., Nicklin M.J.H.;

"The human gene encoding the interleukin-1 receptor (ILIRAP) maps to chromosome 3q28 by fluorescence in and radiation hybrid mapping.";

Genomics 47:325-326(1998).
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
IL-1 receptor accessory protein (Membrane interleukin 1 receptor
                                                                                                                                                                                                                                                                         Huang J., Gao X., Proc. Natl. Acad.
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Primates;
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InterPro; IPR003006; Ig.MHC.
InterPro; IPR004075; ILI_receptor1.
InterPro; IPR000157; TIR_domain.
Pfam; PF00047; ig; 2.
Pfam; PF01582; TIR; 1.
PRINTS; PR01537; INTELKNIRIF.
SMART; SM00409; IG; 2.
SMART; SM00255; TIR; 1.
Q61730;
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01-NOV-1996
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LELKAGL---ENMASRGNINVILVQYKAVKETK--VKELKRAKTVLTVIKWKGEKSKYPQ
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AF167335;
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Pred. No. 5.8e-211;
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J. Biol. Chem. 270:13757-13765 (1995).
EMBL; X85999; CAA59991.1; -.
MGD; MGI:104975; Il1rap.
InterPro; IPR003599; IG.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR003075; TIR_domain.
Pfam; PF00147; ig; 3.
Pfam; PF00047; ig; 3.
Pfam; PF00047; IT; 1.
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SMART; SM00409; IG; 2.
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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Greenfeder S.A., Nunes P., Kwee L., Lab
"Molecular cloning and characterization
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EMBL; U48592; AAB03502.1; -.

Interpro; IPR003559; IS.

Interpro; IPR003006; Ig_MHC.

Interpro; IPR004075; IL1 receptor1.

Interpro; IPR000157; TIR_domain.

Pfam; PP00047; 19; 3.

Pfam; PP001582; TIR; 1.
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MEDLINE=96265355; PubMed=8964912;

Liu C., Chalmers D., Maki R., De Souza E.B.;

"Rat homolog of mouse interleukin-1 receptor accessory cloning, localization and modulation studies.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01537; INTRLKNIR1F SMART; SM00409; IG; 2. SMART; SM00255; TIR; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-JUN-2002
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01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-JUN-2002 (TrEMBLrel. 21, Last annotation
Interleukin-1 receptor accessory protein.
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|||||||||||||||||::||| |
| CSKVAPPLEVVQKDSCFNSPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPSVTWYKG
  LEFKLGVMCQNSIATK----
                                                                                                                                                                                   ACGFGATVLLVVILIVVYHVYWLEMVLFYRAHFGTDETILDGKEYDIYVSYARNAEEEEFF
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                                                                                                                                                                                                                                                                                                                                                                                                   VPPHIYSPNDRVVYEKEPGEELVIPCKVYFSPIMDSHNEIWWTIDGKKPDDVPVDITIIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTEI VNFHNVQPKGMNLSFFI PLVSNNGNYTCVVTYLENGRLFHLTRTMTVKVVGSPKDA
                                                                                                       VLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSPDYVTEKSISM
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75.7%; Pred. No. 8.2e-1
tive 62; Mismatches
                                                                              -LIVVEYRPLEHPHPGILQLKE-----SVSFVSWKGEKSK
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Matches 350
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"IL-1 signaling cascade in liver cells and the involvement of
soluble form of the II-1 receptor accessory protein.";

L. J. Immunol. 164:5277-5286(2000).

R. EMBL; AF167340; AAF71688.1; -.

R. EMBL; AF167335; AAF71688.1; JOINED.

R. EMBL; AF167336; AAF71688.1; JOINED.

R. EMBL; AF167337; AAF71688.1; JOINED.

R. EMBL; AF167339; AAF71688.1; JOINED.

R. EMBL; AF167339; AAF71688.1; JOINED.

R. EMBL; AF167339; AAF71688.1; JOINED.

R. EMBL; AF167339; AAF71688.1; JOINED.

R. InterPro; IFR003599; Ig.

R. InterPro; IFR003599; Ig.

R. InterPro; IFR003599; Ig.

R. F16734; AAF71687.1; -.

R. F16734; AAF71687.1; -.

R. F16735; F16703006; Ig_MHC.

R. F16736; F16703006; Ig_MHC.

R. F16737; SM00409; IG; 2.
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SEQUENCE
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Soluble interleukin 1 receptor accessory protein (Soluble receptor accessory protein).
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Mammalia; Eutheria;
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                           SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQK
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SISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVKQK
                                                                                                          VPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDITIDVTINE
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Primates;
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100.0%; Pred. No. 2.7e-152;
tive 0; Mismatches 0;
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Q1-OCT-2000 (TrEMBLrel. 15, Lr
Q1-OCT-2000 (TrEMBLrel. 21, Lr
Q1-JUN-2002 (TrEMBLrel. 21, Lr
IL1RAPL-2 related protein (Interessory protein-like 2) (TI
IL1RAPL-2 OR IL1R9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JAN-2002) to the EMEL; BC021159; AH121159.1; -.
InterPro; IPR003599; IG.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 3.
SMART; SM00409; IG; 3.
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SEQUENCE
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Mus musculus (Mouse).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
  SEQUENCE
                                           Submitted
                                                              Ferrante
                                                                             TISSUE=ADULT BRAIN;
                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             Q9NP60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYST
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2 (TrEMBLrel. 21, )
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85.1%;
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(TIGIRR-1).
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Pred. No. 7.6e-133;
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                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local Sim
Matches 228;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig like.
InterPro; IPR003006; Ig MHC.
InterPro; IPR004075; IL1 receptor1.
InterPro; IPR000157; TIR_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMMBL; AJ2290436; CAB89867.1; -.
EMBL; AF212016; AAF61307.1; -.
EMBL; AJ272208; CAB86868.1; -.
EMBL; AJ272208; CAB86868.1; -.
EMBL; AF284436; AAG21370.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  class of J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB=BRAIN;
Grabowski M., Lorenz
"A gene (IL1RAPL-2) v
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Sims J.E.;
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TITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LALVVCSVVSTNLKMVSKRNSVDGCIDWSVD-LKTYMALAGEPVRVKCALFYSYIRTNYS
                                                                                                                                                                          TALLITDKPPKPLFPMENQPSVIDVQLGKPLNIPCKAFFGFSGESGPMIYW-MKGEK----
                                                                                                                                                                                                                   VGSPKNAVP-PVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDI
                                                                                                                                                                                                                                                                 DVVWYKECKPKWWRSIIIQKGNALLIQEVQEEDGGNYTCELKY--EGKL--VRRTTELKV
                                                                                                                                                                                                                                                                                                                                                   TYCMKVSMSLTVAENESGLCYNSRIR-----YLEKSEVTKRKEISCPDMDDFKKSDQEP
                                                                                                                                                                                                                                                                                                                                                                                TYCSKVAFPLEVVQKDS--CFNSPMKLPVHKLYIEYG----IQRITCPNVDGYFPSSVKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAHSAGLTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNT
                                                                                                                             TIDVTINESISHSRTEDETR-----TQILSIKKVTSEDLKRSYVCHARSAKGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; PR01537; INTRLKNIRIF,
SM00409; IG; 2.
SM00410; IG like; 1.
SM00255; TIR; 1.
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D.E., Garka K.E.,
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) with
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Pred. No. 2.9e
06; Mismatches
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SM00410; IG_
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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    Matches
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Best Local
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01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                            of the interleukin-1 receptor (IL-IR) class of IL-IR-related proteins based J: Biol. Chem. 275:29946-29954 (2000).
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MEDLINE=20459050; PubMed=10882729;
Born T.L., Smith D.E., Garka K.E.,
Sims J.E.;
                                                                                              SEQUENCE
                                                                                                                  SMART; SM00409; IG;
SMART; SM00410; IG 1
SMART; SM00255; TIR;
                                                                                                                                                                                                                               MGD; MGI:1913106; Illrapl2.
InterPro; IPR003599; Ig.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR000157; TIR_domain.
                                                                                                                                                                                                                                                                                                                                                        EMBL;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of two members of a novel of the interleukin-1 receptor (IL-1R) family. Delineation of a class of IL-1R-related proteins based on signaling.";
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Pfam; PF01582; TIR;
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215;
                                                                                                                                                                                                                                                                                                                                                           AF284437; AAG21371.1; -.
                        Similarity
                                                                                              686 AA;
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    Conservative
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Rodentia;
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Last sequence update)
Last annotation updat
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                                                                                              36160D1CDE9B8264 CRC64;
    Mismatches
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1 MTLLWC-VVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYS 59

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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OT-2000 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
X-linked interleukin-1 receptor accessory protein-like
                                                                                          SEQUENCE FROM N.A.

MEDIJINE-20218565; PubMed=10757639;

Jin H., Viswesvaraiah R., Gardner R.J., Roberts R.

"Two novel members of the interleukin-1 receptor deleted in Xp21.3-Xp21.3 mental retardation.";

Eur. J. Hum. Genet. 8:87-94(2000).

EMBL; AF181284; AAF59411.1;
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C9NZN1
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR004075; III rec;
InterPro; IPR000770; SAND_doi
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
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SMART; SM00408; IGC2; 1.

SMART; SM00258; SAND; 1.

SMART; SM00255; TIR; 1.

Immunoglobulin domain; Receptor.

SEQUENCE 696 AA; 79979 MW; F2EBC371537F9AA0
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PLTSIGNOHTYCNIPMTLINGORPOTKSSREONPDEAHTNSAILPLLPRET
                                                                                                                    LKB-----SVSFVSWKGEKSKHSGSKFWKALRLALPLR-------
                                                                                                                                                        IYVSYAR------NAEEEEFVLLTLRGVLENEFGYKLCIFDRDSLFGGNTVEAVFDF
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                                              FGELQTVSAISMAAATSTALATAHPDLRSTFHNTYHSQMRQKHYYRSYEYDV--PPTGTL
                                                                                           YQEVEALKHTIKLLTVIKWHGPKCNKLNSKFWKRLQYEMPFKRIEPITHEQALDVSEQGP
                                                                                                                                                                                          AYLSYTKVDPDQWNQETGEEERFALEILPDMLEKHYGYKLFIPDRDLIPTGTYIEDVARC
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                                                                                                                                          VDQSKRLIIVMTPNYVVRRGWSI--FELETRLRNMLVTGEIKVILIECSELR----GIMN
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EMBL; AJ243874; CAB56046.1; -.

EMBL; AF284435; AAG31369.1; -.

InterPro; IPR003598; Ig_c2.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR004075; ILI receptor1.

InterPro; IPR000770; SAND_domain.

InterPro; IPR000157; TIR_domain.
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Carrie A., Jun L., Bienvenu T., Vinet M.;
"A new member of the IL-1 receptor family highly expressed
hippocampus and involved in X-linked mental retardation.";
Nat. Genet. 23:25-31(1999)
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SMART; SM00255; TIR; 1.
Immunoglobulin domain.
SEQUENCE 696 AA; 7996
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Pfam; PF01582; TIR; 1.
PRINTS; PR01537; INTRLKN1R1F.
SMART; SM00408; IGc2; 1.
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MEDLINE=20459050; PubMed=10882729;
Smith D.E., Garka K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Identification and characterization of two members of a novel class of the interleukin-1 receptor (IL-1R) family. Delineation of a new class of IL-1R-related proteins based on signaling.";
J. Biol. Chem. 275:29946-29954 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Born T.L., Smith D.E., Sims J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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Mammalia; Eutheria;
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               458
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                                                                                                                                                   DENRVWESDIRI----LKEHLGEQEVSISLI-VDSVEEGDL-GNYSCYVENGNGR--RHAS
                                                                                                                                                                                                                                                                                                                   LILLYATFTQSLKVVTKRGSADGCTDWSID-IKKYQVLVGEPVRIKCALFYGYIRTNYSL
VKQKVPAPRYTVELACGFGATVLLVVILIVVYHVYMLEMVLFYRAHFGTDETILDGKEYD
                                                                                                                                                                                                          -APLIDKPPKILLYPMESKLTIQETQLGDSANLTCRAFFGYSGDVSPLIYWMKGEKFIEDL
                                                                                                                                                                                                                                    GSPKNAVPPVIHSPNDH--VVYEKEPGEBLLIPCTVYFSFLMDSRNBVWWTIDGKKPDDI
                                         AYLSYTKVDPDQWNQETGEEERFALEILPDMLEKHYGYKLFIPDRDLIPTGTYIEDVARC
                                                                   IYVSYAR-----
                                                                                               VLLHKRELMYTVELAGGLGAILLLLVCLVTIYKCYKIEIMLFYRNHFGAEELDGDNKDYD
                                                                                                                                                                             -----TIDVTINESISHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAK 346
                                                                                                                                                                                                                                                                 ILWYKECRTKTWRPSIVFKRDTLLIREVREDDIGNYTCELKY--GGFVVRRTTELTVT--
                                                                                                                                                                                                                                                                                           ITWYMGCYKIQNFNNVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTFHLTRTLTVKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                           --NAEBEFVILTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79968 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.9%; Score 767.5; DB 4; 29.0%; Pred. No. 2.3e-56; tive 127; Mismatches 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9B7A0B503D73CCA9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Renshaw B.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bertles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 696;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
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Q13478;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                     Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96223957; PubMed=8626725;
Parnet P., Garka K.E., Bonnert T.P., Dower S.K., Sims J.E.;
"IL-IRTP is a novel receptor-like molecule similar to the type interleukin-1 receptor and its homologues T1/ST2 and IL-1R AcP.
J. Biol. Chem. 271:3967-3970(1996).
EMBL; U43672; AAC50390.1; -.
HSSP; O60603; IFYW.
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 3. Pfam; PF01582; TIR; 1 PRINTS; PR01537; INTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig.MHC.
InterPro; IPR004075; ILL_receptor1.
InterPro; IPR000157; TIR_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL-1Rrp precursor
                                                                             175
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207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDQSKRLIIVMTPNYVVRRGWSI---FELETRLRNMLVTGEIKVILIECSELR----GIMN
 VEDRSNIVPVLLGPKLNHVAVEL - - GKNVRLNC - -
                                                                            ITWYMGCYKIQNENNVIPB-GMNLSFLIALISNNGNYTCVVTYPENGRTEHLTRTLTVKV
                                                                                                                                                                                    HSAGLTL-IWYWTRODRDLEEPINFRLPENRISKEKDYLWFRPTLLNDTGNYTCMLRNTT 120
                                                                                                                                                                                                               LWVLISV-----
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                                                                                                      Q----KWKLNVIRRNKHSCFTERQVTSKIVEVKKFF----
                                                                                                                               YCSKVAFPLEVVQ--KDSCFN----SPMKLPVHKLYIEYGIQRITCPNVDGYFPSSVKPT
                                                                                                                                                         HEIETTTKSWYKSSGSQEHVB-LNPR-SSSRIALHDCVLEFWPVELNDTGSYFFQMKNYT
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                        VGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDIT
                                                 -SLYKNCKKLLLENNKNPTIKKNAEF----EDQGYYSCVHFLHHNGKLFNITKTENITI
                                                                                                                                                                                                                                                                   174;
                                                                                                                                                                                                                                                                                                                                                              SM00409; IG; 1.
SM00255; TIR; 1
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                                                                                                                                                                                                                                                                                                                      541 AA;
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                                                                                                                                                                                                                                                                                                                      19 P
62304 MW;
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                                                                                                                                                                                                                                                                               14.4%;
                                                                                                                                                                                                                                                                   93;
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                                                                                                                                                                                                                                                                 Score 528; DB 4;
Pred. No. 3.5e-36;
3; Mismatches 215
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Last annotation updat
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; 7173DB9C7EA71D32 CRC64;
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 -SALLNEEDVIYWMFGEENGSDPN
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                                                                                                                                                                                                                                                                    215;
                                                                                                       -QITCEN--SYYQTLVNST
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 260
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                                                                                                                                 Query Match
Best Local Sin
Matches 155;
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Jene 11...

Jene 11...

M81846; ...

M81846; ...

HSSP; P14778; IITB.

InterPro; IPR003599; IG.

InterPro; IPR003006; IG_MHC.

IPR004075; ILl_receptor1.

TPR004074; ILl_receptor1/II.

TPR004074; TIR_domain.
                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                      PRINTS; PRO1536; INTRLKNIR12F
PRINTS; PRO1537; INTRLKNIR1F.
SMART; SM00409; IG; 1.
SMART; SM00255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=92175529; PubMed=1531799;
Guida S., Heguy A., Melli M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL-1 RECEPTOR I.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                 Guida S., Heguy A., Melli M.;
"The chicken IL-1 receptor: differential evolution and extracellular domains.";
Gene 111:239-243(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q90874
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                            Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
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126 AFPLEVVQKDS--CFNSPMKLPVHKLYIBYGIQRITCPNVDGY-FPSSVKPTITWYMGCY
                           55
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                                                                                                       6 CVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTAHSAG
                                              LTLIWYWTRQDRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTYCSKV 125
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                                                                                CVICNYF----
                                                                                                                                               Similarity
                                                                                                                                                                                     20
555 AA;
                                                                                                                                   Conservative
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                                                                                                                                                                                     19 F
555 I
; 63995 MW;
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                              13.5%;
                          -PITTE-RRARIHQRKGLLWFIPAALEDSGLYECEVRSLNRSKQK 109
                                                                                                                                   109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation updat
                                                                                                                                              Score 496;
Pred. No. 1
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                                                                            -----VLVGEPTAISCPV-----ITLPMLHS-D 54
                                                                                                                                   Mismatches
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1.9e-33;
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RESULT 13
Q61098
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                             Query Match
Best Local
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Q61098;
01-NOV-1996 (TrEMBLrel. C
01-NOV-1996 (TrEMBLrel. C
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                             Signal.
                                                                                                                                                                                PRINTS; PR01537; INTRLK
SMART; SM00410; IG like
SMART; SM00255; TIR; 1.
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                                                                                                        SEQUENCE
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Pfam; PF01582; TIR;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interleukin-1 receptor and its hom
J. Biol. Chem. 271:3967-3970(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 QLKESVSFVSWKG---EKSKHSGSKFWKALRLALPLRSLSASSGWNES
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                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:105383;
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                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Garka K.E., Bonnert T.P., Dower is a novel receptor-like molecule
                                                                                                                                                                                                                                                                                                        IPR003600; Ig like.
IPR003006; Ig MHC.
IPR004075; ILI receptor1
IPR000157; TIR domain.
                                                                                                     537 AA;
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61600 MW;
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27.4%;
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Last sequence update)
Last annotation update)
Score 479; DB 11;
Pred. No. 5.1e-32;
2; Mismatches 218
                                                                                                                             POTENTIAL
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                                                                                                        B119FEA403355458 CRC64;
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lecule similar
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and IL-1R AcP.";
                                                  Length
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MTLLWCVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIK---

Matches 167;

Conservative

102;

218;

Indels 122;

Gaps

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Q05208;
01-JUN-1998 (TREMBLRel. 0
01-JUN-1998 (TREMBLRel. 0
01-JUN-2002 (TREMBLRel. 2
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MC.
InterPro; IPR004705; IL1 receptor1. 'InterPro; IPR002052; N6_Mtase.
InterPro; IPR002057; TIR_domain.
Pfam; PP00047; ig; 2.
Pfam; PF01582; TIR; 1.
                                                                                                         MEDILINE=93170492; PubMed=7916701;
Yanagisawa K., Takagi T., Tsukamoto T., Tetsuka T., Tomina "Presence of a novel primary response gene ST2L, encoding highly similar to the interleukin 1 receptor type 1."; PEBS Lett. 318:83-87(1993).
REBL; D13695; BAA02854.1; -.
                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                          ST2L protein precursor. ILIRL1 OR ST2L.
                                                                                               MGD; MGI:98427; Illrl1.
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLFYRRIAERDETLTDGKTYDAFVSYLKECHPENKEEYTFAVETLPRVLEKQFGYKLCIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -RKED-----SSDPNVQEDRKETTTWISEGKLHASKILRFQKITENYLNVLYNCTVANE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRILIVKVVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTID
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                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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21,
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local
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                                                                                                                                    Q9TV71;
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SMART; SN
PROSITE;
 SEQUENCE
Kirisawa
                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin domain; Signal SIGNAL 1 17
                                NCBI_TaxID=9796;
                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                     Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                  Interleukin-1 receptor type
                                                                                                                                                                                                             538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LW--CVVSLYFYGILQSDASERCDDWGLDTMRQIQVFEDEPARIKCPLFEHFLKFNYSTA 61
                                                                                                                                                                                                                                   LALPL-RSLSASSGWNESCSSQSDISLDH
                                                                                                                                                                                                                                                                                                                                                                                                          LEYDCLALNLHGMIRHTIRLRRKQPIDHRSIYYIVAGCSLLLMFINVLVIVLKVFWIBVA
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                                                                                                                                                                                                                                                             --SKVILIEMEPLGEASRLQVGDLQDSLQHLVKIQGTIKWREDHVADKQSLSSKFWKHVR
                                                                                                                                                                                                                                                                                  IATKLIVVEYRPL-EHPHPGILQLKESVSF-----VSWKGE--KSKHS-GSKFWKALR
                                                                                                                                                                                                                                                                                                                                                             LFWRDIVTPYKTRNDGKLYDAYIIYPRVFRGSAAGTHSVEYFVHHTLPDVLENKCGYKLC
                                                                                                                                                                                                                                                                                                                                                                                                                                    RSYVCHARSAKGEVAKAAKVKOKVPAPRYTV-ELACGFGATVLLVVILIVVYHVYWLEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWWTIDGKKPDDITIDVTINESISHSRTEDE-----TRTQILSIKKVTSEDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLTRTLTVKVVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFS----FLMDSRNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITWYMGCYKION------FINIVIPEGMNLSFLIALISNNGNYTCVVTYPENGRTF
                                                                                                                                                                                                             YQMPVPERASKTASVAAPLSGKACLDLKH
                                                                                                                                                                                                                                                                                                            IYGRDLLPGQDAATVVESSIQNSRRQVFVLAPHMMHSKEFAYEQEIAL----HSALIQNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVTATRSFTVEEKGPSMFPVITNPPYNHTM-EVEIGKPASIACSACFGKGSHFLAD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKTGYLNVTIHKKPPSCNIPD-----YLMYSTVRGSDKNFKITCPTIDLY---NWTAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSKVAFPLEVVQKDSCFNSPMKLPVHKLYIEYGIQR-----ITCPNVDGYFPSSVKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSAGLTLIWYWTRODRDLEEPINFRLPENRISKEKDVLWFRPTLLNDTGNYTCMLRNTTY 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWALAILTLPMY-LTVTEGSK--SSWGL------ENEALIVRCP-----QRGRST-
                                                                                                                                                                                                                                                                                                                                     IFDRDSLPGGNTVEAVFDFIQRSRRMIVVLSP-----DYVTEKSISMLEFKLGVMCQNS
                                                                                                                                                                                                                                                                                                                                                                                    LFYRAHFGTDETILDGKEYDIYVSYAR-----
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SM00255; TIR; 1.
E; PS00092; NG_MTASE; UNKNOWN_1.
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          FROM N.A.
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567 j
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                                                                                                                                                 PRELIMINARY;
Hashimoto
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                                            Chordata; Craniata; Vert
Perissodactyla; Equidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64801 MW;
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25.9%;
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 Sakamoto
                                                                                             Last sequence update)
                                                                                  I precursor.
                                                                                                                      Created)
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Pred. No. 6.7e-32;
5; Mismatches 227
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                                                                                                                                                                                                                                                                                                                                                                          -NAEEEEFVLLTLRGVLENEFGYKLC
                                                            Vertebrata;
 Enya
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 Hagiwara
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                                                            Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Juery Match 13.0%; Score 477.5; DB 6; Length 573; Best Local Similarity 25.8%; Pred. No. 7.5e-32; Matches 153; Conservative 120; Mismatches 224; Indels 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01537; INTRLKONIRIP SMART; SM00410; IG like; 2. SMART; SM00255; TIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AB020338; BAA83730.1; -. HSSP; P14778; 1IRA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01538; INTRLEUKNIR1.
PRINTS; PR01536; INTRLKNIR12F.
                                                                                                                                                                                                                                                                                              270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     deceptor;
                                                                                                                                           384 TYDAYILYPKILGEGSTSNSDIFVFKVLPEVLEKQCGYKLFIYGRDDYVGEDIVEVTNEN 443
                                                                                                                                                                                                                       329
                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 WYMGCYK--IQNENNVIPEGMNLSFLIALI--SNNGNYTCVVTYPENGRTFHLTRTLTVK 232
   498
                                                                                                            458
                                                                                                                                                                                   404
                                                                                                                                                                                                                                                     349 QKVPAPRYTVELACGFGATVLLVVIL---IVVYHVYWLEMVLFYR--AHFGTDETILDGK 403
                                                                                                                                                                                                                                                                                                                              293 TIDVTINESI----SHSRTEDETRTQILSIKKVTSEDLKRSYVCHARSAKGEVAKAAKVK 348
                                                                                                                                                                                                                                                                                                                                                                217 TLDEIRPTKPLIVSPVNB--TMEVDLGSQVQLICNVTGMF----TDFVYWRWNGSLIDD- 269
                                                                                                                                                                                                                                                                                                                                                                                                     233 VVGSPKNAVPPVIHSPNDHVVYEKEPGEELLIPCTVYFSFLMDSRNEVWWTIDGKKPDDI 292
                                                                                                                                                                                                                                                                                                                                                                                                                                         160 WYKDCQPLLLDNINFI---GKTDKLIVANVTEAHKGHYTCHISYTHLGKQYPITKVIGLI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 KVKITARFVOHEPDLCYNAOAIFTOKLPLG----EDGL--LVCPYLEVFRDENNELPKIO 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 KVAFPLEVVQ--KDSCFNS----PMKLPVHKLYIEYGIQRITCPNVDGYFPSSVK-PTIT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fam; PF00047; ig; 2 fam; PF01582; TIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S1 SNGTTIWY----KNDSETPVSME-RDSRIHQYKDKLWFVPAKIEDSGHYYCAVRNSTYCL 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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                                                                                                                                                                             EYDIYVSYAR-----NAESEEFVLLTLRGVLENEFGYKLCIFDRDSLPGGNTVEAVFDF 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGLILIWYWIRQDRDLBEPINFRLPENRISKEKOVLWFRPTLLNDTGNYTCMLRNTTYCS 123
                    PGILQLKESVSFVS------WKGEKSK---HSGSKFWKALRLALPLRSLSASS 553
                                                                    IKKSRRLIIILVRETSGLSWLGSSSEEQIAM----YNALVQDGI--KIILLELEKIQDYE
                                                                                           IQRSRRMIVVLSPD-----YVTEKSISMLEFKLGVMCQNSIATKLIVVEYRPLEHPH 509
                                                                                                                                                                                                                 -SDPVLVEEYKPVENPSLKRRHTLITVLNISAVESRFYLYPFTCLAKNSYGRSAAYVQLR 328
----KMPESIKFIKRKHGALRWSGDSRKGPQSAKARFWKNVRYRMPVQRQLPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o; IPR003600; Ig_like.
j; IPR003006; Ig_MHC.
s; IPR003076; ILIR_receptor.
j; IPR004075; ILI_receptor1..
j; IPR004074; ILI_receptor1/II.
j; IPR000157; TIR_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 573
573 AA; 65766 MW;
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573
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MATURE INTERLEUKIN-1 RECEPTOR TYPE I.
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Search completed: April 23, 2003; 08:54:00 Job time: 100 secs